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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:10:37 ; Search time 30.1562 Seconds
(without alignments)
2279.856 Million cell updates/sec

Title: US-10-697-894-39
Perfect score: 4781
Sequence: 1 MRQPASRDLPQBPVPG.....VPLDGRAPINGCCSLDAE 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/aaa/5A-COMB.pep:*

2: /cgn2_6/prodata/1/aaa/5B-COMB.pep:*

3: /cgn2_6/prodata/1/aaa/6A-COMB.pep:*

4: /cgn2_6/prodata/1/aaa/6B-COMB.pep:*

5: /cgn2_6/prodata/1/aaa/PCTUS-COMB.pep:*

6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	1	US-07-872-644-39 Sequence 39, Appl
2	4781	100.0	921	1	US-08-297-494-39 Sequence 39, Appl
3	4781	100.0	921	1	US-08-297-510-39 Sequence 39, Appl
4	4781	100.0	921	1	US-08-479-532-39 Sequence 39, Appl
5	4781	100.0	921	1	US-08-455-526-39 Sequence 39, Appl
6	4781	100.0	921	1	US-08-455-525-39 Sequence 39, Appl
7	4781	100.0	921	3	US-09-139-491-39 Sequence 39, Appl
8	4781	100.0	921	3	US-09-754-250-5 Sequence 5, Appl
9	4781	100.0	921	5	PCT-US92-03222-39 Sequence 39, Appl
10	4781	100.0	921	5	PCT-US92-03222-39 Sequence 39, Appl
11	4657	97.4	942	1	US-07-872-644-43 Sequence 43, Appl
12	4657	97.4	942	1	US-08-297-494-43 Sequence 43, Appl
13	4657	97.4	942	1	US-08-297-510-43 Sequence 43, Appl
14	4657	97.4	942	1	US-08-479-532-43 Sequence 43, Appl
15	4657	97.4	942	1	US-08-455-526-43 Sequence 43, Appl
16	4657	97.4	942	1	US-08-455-525-43 Sequence 43, Appl
17	4657	97.4	942	3	US-09-139-491-43 Sequence 43, Appl
18	4657	97.4	942	4	US-09-883-825-43 Sequence 43, Appl
19	4657	97.4	942	5	PCT-US92-03222-43 Sequence 43, Appl
20	4533.5	94.8	920	3	US-09-754-250-2 Sequence 2, Appl
21	4474.5	93.6	941	1	US-07-872-644-45 Sequence 45, Appl
22	4474.5	93.6	941	1	US-08-297-494-45 Sequence 45, Appl
23	4474.5	93.6	941	1	US-08-297-510-45 Sequence 45, Appl
24	4474.5	93.6	941	1	US-08-479-532-45 Sequence 45, Appl
25	4474.5	93.6	941	1	US-08-455-526-45 Sequence 45, Appl
26	4474.5	93.6	941	1	US-08-455-525-45 Sequence 45, Appl
27	4474.5	93.6	941	3	US-09-139-491-45 Sequence 45, Appl

28	4474.5	93.6	941	4	US-09-883-825-45 Sequence 45, Appl
29	4474.5	93.6	941	4	US-09-708-392-5 Sequence 5, Appl
30	4474.5	93.6	941	4	US-09-949-016-6244 Sequence 6244, Ap
31	4474.5	93.6	941	5	PCT-US92-03222-45 Sequence 45, Appl
32	4473.5	93.6	905	3	US-09-754-250-4 Sequence 4, Appl
33	3698	77.3	802	4	US-09-949-016-7922 Sequence 7922, Ap
34	914.5	19.1	779	2	US-08-951-648-6 Sequence 6, Appl
35	914.5	19.1	779	3	US-09-174-437-6 Sequence 6, Appl
36	914.5	19.1	779	4	US-09-686-055A-6 Sequence 1, Appl
37	914.5	19.1	779	4	US-09-420-190-1 Sequence 1, Appl
38	913	19.1	803	2	US-08-951-648-4 Sequence 4, Appl
39	913	19.1	803	3	US-09-174-437-4 Sequence 4, Appl
40	913	19.1	803	3	US-09-686-055A-4 Sequence 4, Appl
41	912.5	19.1	766	3	US-08-951-648-2 Sequence 2, Appl
42	912.5	19.1	766	3	US-09-174-437-2 Sequence 2, Appl
43	912.5	19.1	766	4	US-09-686-055A-2 Sequence 2, Appl
44	801	16.8	875	1	US-08-480-547A-23 Sequence 23, Appl
45	801	16.8	875	1	US-08-250-847B-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-07-872-644-39
; Sequence 39, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-39

Query Match 100.0%; Score 4781; DB 1; Length 921;

Best Local Similarity 100.0%; Pred. No. 0;			
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MRROPAASRDLPFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLPKVETV	60
Db	1	MRROPAASRDLPFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLPKVETV	60
Qy	61	YTYLLDGSRLVCEPPELPOEGKVRKREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAP	120
Db	61	YTYLLDGSRLVCEPPELPOEGKVRKREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAP	120
Qy	121	DTQVLVPLVDKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV	180
Db	121	DTQVLVPLVDKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV	180
Qy	181	APQATONPPEAAGDKGGVAYTNQDRKILQICGELYDLQDASSLQKLVQLOQETQASR	240
Db	181	APQATONPPEAAGDKGGVAYTNQDRKILQICGELYDLQDASSLQKLVQLOQETQASR	240
Qy	241	CCLLLVSDNLQLSCKVIGDKVLEEEISFPITTTGRLGQGVVEDKKSILQKDLTSDMQOQL	300
Db	241	CCLLLVSDNLQLSCKVIGDKVLEEEISFPITTTGRLGQGVVEDKKSILQKDLTSDMQOQL	300
Qy	301	SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTST	360
Db	301	SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTST	360
Qy	361	LAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420
Db	361	LAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420
Qy	421	VAKVFDGSGVDESEYIIRIPADQGIAGHVATTGQILNIPDAVAPLFRGVDDSTGRTR	480
Db	421	VAKVFDGSGVDESEYIIRIPADQGIAGHVATTGQILNIPDAVAPLFRGVDDSTGRTR	480
Qy	481	NILCFPIKNEQVIGVLAELNKGMPFSKFDDELATAFSIYCGISIAHSLLYKKNVNEA	540
Db	481	NILCFPIKNEQVIGVLAELNKGMPFSKFDDELATAFSIYCGISIAHSLLYKKNVNEA	540
Qy	541	QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTVTPRSLPEDDTSMAIL	600
Db	541	QYRSHLANEMMYHMKVSDDEYTKLLHDGIPQVAAIDSNFASFTVTPRSLPEDDTSMAIL	600
Qy	601	SMLODMFPIKYNKIDCPTLAPFCLMVKGYRDPVYHNMHAFSVSHFCYLLYKNLELTYN	660
Db	601	SMLODMFPIKYNKIDCPTLAPFCLMVKGYRDPVYHNMHAFSVSHFCYLLYKNLELTYN	660
Qy	661	LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGVSMEHRRHFAQAIAIINT	720
Db	661	LEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALYSSEGVSMEHRRHFAQAIAIINT	720
Qy	721	HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHHSLLL	780
Db	721	HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIIPKDLQMAEVGYDRTNKQHHSLLL	780
Qy	781	CLMTSCDLSQTKGWKTRKIAELIYKEPFSQGDLEKAMGNRPMENMDREKAYIPELQI	840
Db	781	CLMTSCDLSQTKGWKTRKIAELIYKEPFSQGDLEKAMGNRPMENMDREKAYIPELQI	840
Qy	841	SFMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLPSSNLSDFLDEEY	900
Db	841	SFMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLPSSNLSDFLDEEY	900
Qy	901	EVPLDGGARAPINGCCSLDAE 921	
Db	901	EVPLDGGARAPINGCCSLDAE 921	

RESULT 2
US-08-297-494-39
; Sequence 39, Application us/08297494
; Patent No. 5580771
; GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,494
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5580771and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-297-494-39

Query Match 100.0%; Score 4781; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRROPAASRDLPFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLPKVETV	60
Db	1	MRROPAASRDLPFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQQAQVKEALSAPLPKVETV	60
Qy	61	YTYLLDGSRLVCEPPELPOEGKVRKREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAP	120
Db	61	YTYLLDGSRLVCEPPELPOEGKVRKREAVISRKRLGCGNLGSPDLPGKPLARLVAPLAP	120
Qy	121	DTQVLVPLVDKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV	180
Db	121	DTQVLVPLVDKEAGAAVAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQOQRESSV	180
Qy	181	APQATONPPEAAGDKGGVAYTNQDRKILQICGELYDLQDASSLQKLVQLOQETQASR	240
Db	181	APQATONPPEAAGDKGGVAYTNQDRKILQICGELYDLQDASSLQKLVQLOQETQASR	240
Qy	241	CCLLLVSDNLQLSCKVIGDKVLEEEISFPITTTGRLGQGVVEDKKSILQKDLTSDMQOQL	300
Db	241	CCLLLVSDNLQLSCKVIGDKVLEEEISFPITTTGRLGQGVVEDKKSILQKDLTSDMQOQL	300
Qy	301	SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTST	360
Db	301	SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTST	360
Qy	361	LAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL	420

Db 361 LAFOKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy 481 NILCPPIKNEQVEIGVLAELVKNKINGPWFSEKDEDLATAFISYICGSIASHSLLYKKVNEA 540
Db 481 NILCPPIKNEQVEIGVLAELVKNKINGPWFSEKDEDLATAFISYICGSIASHSLLYKKVNEA 540
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNMHAFSVSHFCYLLYKNLELTY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNMHAFSVSHFCYLLYKNLELTY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
Qy 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSLLL 780
Db 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSLLL 780
Qy 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOI 840
Db 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOI 840
Qy 841 SPMEHAMPIYKXLQDLFPKAAELYERVAENRHTKVSHTKFTIRGLPSNNSLDPLDBEY 900
Db 841 SPMEHAMPIYKXLQDLFPKAAELYERVAENRHTKVSHTKFTIRGLPSNNSLDPLDBEY 900
Qy 901 EVDPLDGRAPINGCCSLDAE 921
Db 901 EVDPLDGRAPINGCCSLDAE 921

RESULT 3

US-08-297-510-39
; Sequence 39, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-297-510-39

Query Match 100.0%; Score 4781; DB 1; Length 921;
Beat Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRRQPAASRDLPFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKQVTV 60
Db 1 MRRQPAASRDLPFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKQVTV 60
Qy 61 YTYLLDGSRLVCEPPELPHQEGKQREAVISRKELGCGNGLGPDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEPPELPHQEGKQREAVISRKELGCGNGLGPDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVIPLVDKEAGAAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQOQRESSV 180
Db 121 DTQVLVIPLVDKEAGAAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQOQRESSV 180
Qy 181 APEATQNPPEAAGDQKGVAYTNQDKILQCGELYDLDDASSLQKVLQYLOQFTQASR 240
Db 181 APEATQNPPEAAGDQKGVAYTNQDKILQCGELYDLDDASSLQKVLQYLOQFTQASR 240
Qy 241 CCLLLVSDNLQLSCKVIGDKVLEESISFPLTTGRGLQGVEDKKIOLKOLTSQDMQQLQ 300
Db 241 CCLLLVSDNLQLSCKVIGDKVLEESISFPLTTGRGLQGVEDKKIOLKOLTSQDMQQLQ 300
Qy 301 SMLGCEVOAMLCVPVISRATQVVALACAFNKLGGDLFTDDEHVIOHCFTHTSVLTST 360
Db 301 SMLGCEVOAMLCVPVISRATQVVALACAFNKLGGDLFTDDEHVIOHCFTHTSVLTST 360
Qy 361 LAFQKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420
Db 361 LAFQKEQKLCQKQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420
Qy 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy 481 NILCPPIKNEQVEIGVLAELVKNKINGPWFSEKDEDLATAFISYICGSIASHSLLYKKVNEA 540
Db 481 NILCPPIKNEQVEIGVLAELVKNKINGPWFSEKDEDLATAFISYICGSIASHSLLYKKVNEA 540
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNMHAFSVSHFCYLLYKNLELTY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNMHAFSVSHFCYLLYKNLELTY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
Qy 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSLLL 780
Db 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQKMAEVGYDRTNKHSLLL 780
Qy 781 CLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELOI 840

Db 781 CLMTSCDSDQTKGKTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTVKSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTVKSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVDPLDGRAPINGCCSLDAE 921
Db 901 EVDPLDGRAPINGCCSLDAE 921

RESULT 4
US-08-479-532-39
; Sequence 39, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-532-39

Query Match 100.0%; Score 4781; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQAVKEALSAVLPKVETV 60
Db 1 MRQPAASRDIFAQEPVPPGSGDGLQDALLSLGSDVIDVAGLQAVKEALSAVLPKVETV 60
Qy 61 YTYLLDGSRLVCEPPHLPQEGKVRNAVTSRKLGCNGLGSPDLPGKPLARLVAPLAP 120

Db 61 YTYLLDGSRLVCEPPHLPQEGKVRNAVTSRKLGCNGLGSPDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLOAVEKHTLVALKRVQALQORESSV 180
Qy 181 APEATQPPPEAAGDQGGVAYTNODRKILQLCCGELYDLDDASSLQQLVQLQOETOASR 240
Db 181 APEATQPPPEAAGDQGGVAYTNODRKILQLCCGELYDLDDASSLQQLVQLQOETOASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKLTSEDMMQLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDKKSIQLKLTSEDMMQLQ 300
Qy 301 SMLGCEVOAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLVTS 360
Db 301 SMLGCEVOAMLCVPVISRATDQVVVALACAFNKLGGDLFTDQDEHVIQHCFTYTTVLVTS 360
Qy 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLQOEIITEARNLSNAEICSVFLLDONEL 420
Db 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLQOEIITEARNLSNAEICSVFLLDONEL 420
Qy 421 VAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy 481 NILCFPIKNENQEVIGVAELVKNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKNEA 540
Db 481 NILCFPIKNENQEVIGVAELVKNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKNEA 540
Qy 541 QYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMHAFSVSHFCYLLYKNLELTYN 660
Db 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMHAFSVSHFCYLLYKNLELTYN 660
Qy 661 LEDMEIFALFISCMCHDLHRGTNNSPQVASKSVLAALYSSEGSVMRHHFPAQAIINT 720
Db 661 LEDMEIFALFISCMCHDLHRGTNNSPQVASKSVLAALYSSEGSVMRHHFPAQAIINT 720
Qy 721 HGCNIPDHFSDKYQRMDLMDRIILATDLAHLIRIFKDLQKMAEVGYDRTNKHSLLL 780
Db 721 HGCNIPDHFSDKYQRMDLMDRIILATDLAHLIRIFKDLQKMAEVGYDRTNKHSLLL 780
Qy 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
Db 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTVKSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTVKSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVDPLDGRAPINGCCSLDAE 921
Db 901 EVDPLDGRAPINGCCSLDAE 921

RESULT 5
US-08-455-526-39
; Sequence 39, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,526
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494
FILING DATE: 29-AUG-1994
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5789553and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-526-39

Query Match 100.0%; Score 4781; DB 1; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRQPAASRDLPQAPVPVPGSGDGLQDALLSLGSLVQVAGLQVAVKALSAVLKPVETV 60
DB 1 MRQPAASRDLPQAPVPVPGSGDGLQDALLSLGSLVQVAGLQVAVKALSAVLKPVETV 60

QY 61 YTYLLDGSRLVCEPPHLPQEGKVRVAVSRKLGCGNGLGPSDLPGKPLARLVAPLAP 120
DB 61 YTYLLDGSRLVCEPPHLPQEGKVRVAVSRKLGCGNGLGPSDLPGKPLARLVAPLAP 120

QY 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
DB 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180

QY 181 APEATONPPEAAGDQKGVAVTNQDKTLQCGELYLDASSLQKVLQYLOQTQASR 240
DB 181 APEATONPPEAAGDQKGVAVTNQDKTLQCGELYLDASSLQKVLQYLOQTQASR 240

QY 241 CCLLVSEDLNQLSKVIGDKVLEBEISPLTTGRLGVQVEDKKSQKLTSEDMDQQLQ 300
DB 241 CCLLVSEDLNQLSKVIGDKVLEBEISPLTTGRLGVQVEDKKSQKLTSEDMDQQLQ 300

QY 301 SMLGCEVQAMLCPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSVLST 360
DB 301 SMLGCEVQAMLCPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSVLST 360

QY 361 LAFQKEQKLKCCQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420
DB 361 LAFQKEQKLKCCQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQNEL 420

QY 421 VAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIPDAYAHLFVRGVDDSDGFRTR 480
DB 421 VAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIPDAYAHLFVRGVDDSDGFRTR 480

QY 481 NILCPPIKNENQEVIGVAELVNKINGPWFSPKDEDLATAFSYICGSIASHSLYKKNFA 540
DB 481 NILCPPIKNENQEVIGVAELVNKINGPWFSPKDEDLATAFSYICGSIASHSLYKKNFA 540

QY 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAIDSNFASFTYTPRSLPDDTSMAIL 600
DB 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAIDSNFASFTYTPRSLPDDTSMAIL 600

QY 601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNMWHAFSVSHFCYLLYKNLELTY 660
DB 601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNMWHAFSVSHFCYLLYKNLELTY 660

QY 661 LEDMBIPALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPAQAILNT 720
DB 661 LEDMBIPALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPAQAILNT 720

QY 721 HGCNIFDHFSRKDYORMLDLMRDIIATDLAHLRIFKDLQKMAEVDYRTNKHSLLL 780
DB 721 HGCNIFDHFSRKDYORMLDLMRDIIATDLAHLRIFKDLQKMAEVDYRTNKHSLLL 780

QY 781 CLLMTSCDLSQTKGKWTTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
DB 781 CLLMTSCDLSQTKGKWTTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840

QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
DB 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900

QY 901 EVPDLGAPINGCCSLDAE 921
DB 901 EVPDLGAPINGCCSLDAE 921

RESULT 6
US-08-455-525-39
; Sequence 39, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:

Db 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
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Db 181 APEATONPPEEAGDGKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOETQASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKSKISQLKDLTSEDNQQLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKSKISQLKDLTSEDNQQLQ 300
Qy 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360
Db 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360
Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420
Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420
Qy 421 VAKVFDGGVVEDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
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Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTVTPRSLPDDTSMALL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTVTPRSLPDDTSMALL 600
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHPFSVSHFVLLYKNLELTY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHPFSVSHFVLLYKNLELTY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720
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Db 721 HGCNIFDHFSRKDYQRMULDARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
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Db 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVPDLGAPINGCCSLDAE 921
Db 901 EVPDLGAPINGCCSLDAE 921

RESULT 8
US-09-754-250-5
; Sequence 5, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO01063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 921
; TYPE: PRT

; ORGANISM: Bos taurus
US-09-754-250-5
Query Match 100.0%; Score 4781; DB 3; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRRQPAASRDLPQAQSPVPPSGDGLAQDALLSLGSLVDAQGLQAAVKEALSAPLKVETV 60
Db 1 MRRQPAASRDLPQAQSPVPPSGDGLAQDALLSLGSLVDAQGLQAAVKEALSAPLKVETV 60
Qy 61 YTYLLDGSRLVCEPPELPOEGKVRVAVISRKLGCGNGLGSPDLPGKPLARLAPLAP 120
Db 61 YTYLLDGSRLVCEPPELPOEGKVRVAVISRKLGCGNGLGSPDLPGKPLARLAPLAP 120
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Qy 181 APEATONPPEEAGDGKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOETQASR 240
Db 181 APEATONPPEEAGDGKGGVAVTNQDRKILQLCGELYDLDDASSLQQLKVLQYLQOETQASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKSKISQLKDLTSEDNQQLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEBISFPPLTTGRLGQVVEDKSKISQLKDLTSEDNQQLQ 300
Qy 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360
Db 301 SMLGCEVQAMLCVPVISRATDOVVACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST 360
Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420
Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLLDQNEL 420
Qy 421 VAKVFDGGVVEDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Qy 481 NILCPPIKNEQEVIGVAELVNKINGPWFSEKFEDEDLATAFSYCGISIAHSLLYKKVNEA 540
Db 481 NILCPPIKNEQEVIGVAELVNKINGPWFSEKFEDEDLATAFSYCGISIAHSLLYKKVNEA 540
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTVTPRSLPDDTSMALL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSNFASFTVTPRSLPDDTSMALL 600
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHPFSVSHFVLLYKNLELTY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWHPFSVSHFVLLYKNLELTY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHFAQAIANT 720
Qy 721 HGCNIFDHFSRKDYQRMULDARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
Db 721 HGCNIFDHFSRKDYQRMULDARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
Qy 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
Db 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVPDLGAPINGCCSLDAE 921
Db 901 EVPDLGAPINGCCSLDAE 921

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US-09-883-825-39
; Sequence 39, Application US/09883825
; Patent No. 6842040
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6642040and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 921 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-883-825-39
Query Match 100.0%; Score 4781; DB 4; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRQPAAASRDLEFAQEPVPPGSGDQALQDALLSLGSLVDVAGLQQAQVKEALSAVLPKVETV 60
Db 1 MRQPAAASRDLEFAQEPVPPGSGDQALQDALLSLGSLVDVAGLQQAQVKEALSAVLPKVETV 60
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Db 61 YTYLLDGSRLVCEPPELHPQEGKVRNAVLSRKLGCNGLGPSDLPGKPLARLVAPLAP 120
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Db 181 APEATQNPPEAAGDQKGVAATYQDRKILQLCGELYDLDASSLQLKVLQYLOQETQASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGOVVEDKKSIOQLKDLTSEDMOQLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGOVVEDKKSIOQLKDLTSEDMOQLQ 300
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Db 361 LAFQEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy 421 VAKVFDGGVDEDSYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSGFRTR 480
Db 421 VAKVFDGGVDEDSYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSGFRTR 480
Qy 481 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
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Qy 661 LEDMEIFALFISCMCHDLHRGTNNSPQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
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Qy 781 CLLMTSCDLSDOTGKWTTRKIAELIYKEPFSQGLKAMGNRPMEMMDREKAVIPELQI 840
Db 781 CLLMTSCDLSDOTGKWTTRKIAELIYKEPFSQGLKAMGNRPMEMMDREKAVIPELQI 840
Qy 841 SFMEHIAMPYIKLQDLFPKAAELYERVANSRHWTKVSHKFTTIRGLPSNNSLDFLDEEY 900
Db 841 SFMEHIAMPYIKLQDLFPKAAELYERVANSRHWTKVSHKFTTIRGLPSNNSLDFLDEEY 900
Qy 901 EVDPLDGAAPINGCCCSLDAE 921
Db 901 EVDPLDGAAPINGCCCSLDAE 921
RESULT 10
PCT-US92-03222-39
; Sequence 39, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/03222
;; FILING DATE: 19920420
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/688,356
;; FILING DATE: 04-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Noland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/30822
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 346-5750
;; TELEFAX: (312) 984-9740
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 39:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 921 amino acids
;; TYPE: AMINO ACID
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US92-03222-39

Query Match 100.0%; Score 4781; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRQPAAASRDLPQAPVPPGSDGALQDALLSLGSDVIVAGIQQAAVKEALSAVLPKVTY 60
Db 1 MRQPAAASRDLPQAPVPPGSDGALQDALLSLGSDVIVAGIQQAAVKEALSAVLPKVTY 60

Qy 61 YTYLDDGSRLCEBPPEHPHLPQEGKRVREAVISRKRGCGNGLGSPDLPGKPLARLVAPLAP 120
Db 61 YTYLDDGSRLCEBPPEHPHLPQEGKRVREAVISRKRGCGNGLGSPDLPGKPLARLVAPLAP 120

Qy 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEBSLQAVEKHITLVALKRVQALQORESSV 180
Db 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEBSLQAVEKHITLVALKRVQALQORESSV 180

Qy 181 APEATONPEEAAGDQKGVAVTNDQRKTLQCGELYDLDASSLQQLKVLQYLOQTQASR 240
Db 181 APEATONPEEAAGDQKGVAVTNDQRKTLQCGELYDLDASSLQQLKVLQYLOQTQASR 240

Qy 241 CCLLVSEDNLQLSCKVIGDKVLEBIEISFPLTTGRIGQVVEDKSGIQKDLTSEDMDQQLQ 300
Db 241 CCLLVSEDNLQLSCKVIGDKVLEBIEISFPLTTGRIGQVVEDKSGIQKDLTSEDMDQQLQ 300

Qy 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360
Db 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360

Qy 361 LAFOKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFOKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420

Qy 421 VAKVFDGGVVEDESEIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSGTGFTR 480
Db 421 VAKVFDGGVVEDESEIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSGTGFTR 480

Qy 481 NILCFPIKNQEVIGVAELVNKINGPWFSPKFEDELATAFSIYCGISIAHSLLYKKVNEA 540
Db 481 NILCFPIKNQEVIGVAELVNKINGPWFSPKFEDELATAFSIYCGISIAHSLLYKKVNEA 540

Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAIDSNFASFTYTPRSLPEDDTSMAIL 600

Qy 601 SMLQDMFINNYKIDCPTLARFCLMVKGYRDPYPYHNMWHPFSVSHFCVLLYKNELTNY 660
Db 601 SMLQDMFINNYKIDCPTLARFCLMVKGYRDPYPYHNMWHPFSVSHFCVLLYKNELTNY 660

Qy 661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSBGSVYMERHFFAQAIILNT 720

Db 661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSBGSVYMERHFFAQAIILNT 720
Qy 721 HGCNIFDHFSDKDYQRMULDLMRDIIILATDLAHLHRIFKDLQKMAEYGYDRTNKQHSLLL 780
Db 721 HGCNIFDHFSDKDYQRMULDLMRDIIILATDLAHLHRIFKDLQKMAEYGYDRTNKQHSLLL 780

Qy 781 CLMTSCDLSQDTKGWTKTKIARLIYKFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
Db 781 CLMTSCDLSQDTKGWTKTKIARLIYKFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840

Qy 841 SPMEHIAMPIYKLLQDLFPKAAELYERVASNEHHTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SPMEHIAMPIYKLLQDLFPKAAELYERVASNEHHTKVSHKFTIRGLPSNNSLDFLDEY 900

Qy 901 EVPDLGAPINGCCSLDAE 921
Db 901 EVPDLGAPINGCCSLDAE 921

RESULT 11
US-07-872-644-43
; Sequence 43, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell,
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-43

Query Match 97.4%; Score 4657; DB 1; Length 942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 434 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCPFKENOE 493
Db 455 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCPFKENOE 514
QY 494 VIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 634
QY 614 IDCPTLARFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYNLNTLYLEDMEIFALFISC 673
Db 635 IDCPTLARFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYNLNTLYLEDMEIFALFISC 694
QY 674 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHFAQAIALINTHGCNIFDHF SRKD 733
Db 695 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHFAQAIALINTHGCNIFDHF SRKD 754
QY 734 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVDRTNKQHSLLCLLMTSCDLSDDT 793
Db 755 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVDRTNKQHSLLCLLMTSCDLSDDT 814
QY 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIAMPYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIAMPYKL 874
QY 854 LODLFPKAAELYERVASNEHWTKVSHKFTIRGLPSNNSLDPLDEYEVDPDLDGARAPIN 913
Db 875 LODLFPKAAELYERVASNEHWTKVSHKFTIRGLPSNNSLDPLDEYEVDPDLDGARAPIN 934
QY 914 GCCSLDAE 921
Db 935 GCCSLDAE 942

RESULT 13
US-08-297-510-43
; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Bevo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-297-510-43

Query Match 97.4%; Score 4657; DB 1; Length 942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 14 QSPVPGSGDQALDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 73
Db 35 EPPPPPPQCADSLQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC 94
QY 74 EPPHELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLVAPLAPDTQVLVPLVDXE 133
Db 95 EPPHELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLVAPLAPDTQVLVPLVDXE 154
QY 134 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA 193
Db 155 AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA 214
QY 194 GQKGGVATYTDQDKILQCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSENLQL 253
Db 215 GQKGGVATYTDQDKILQCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSENLQL 274
QY 254 SCKVIGDKVLEEEISFPPLTTGRIGQVVEDKGIQKDLTSEDVQQLQSMGCEVQAMLCV 313
Db 275 SCKVIGDKVLEEEISFPPLTTGRIGQVVEDKGIQKDLTSEDVQQLQSMGCEVQAMLCV 334
QY 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 373
Db 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQKEQKLKCEC 394
QY 374 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNABEICSVFLLDDONELVAKVDFGGVVEDE 433
Db 395 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNABEICSVFLLDDONELVAKVDFGGVVEDE 454
QY 434 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCPFKENOE 493
Db 455 SYEIRIPADOGIAGHVATTGQIILNIPDAYAHPLPYRGVDDSTGFRTRNLTCPFKENOE 514
QY 494 VIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 634
QY 614 IDCPTLARFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYNLNTLYLEDMEIFALFISC 673
Db 635 IDCPTLARFCLMVKGYRDPYPVHNMHAFSVSHFCYLLYNLNTLYLEDMEIFALFISC 694
QY 674 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHFAQAIALINTHGCNIFDHF SRKD 733
Db 695 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHFAQAIALINTHGCNIFDHF SRKD 754
QY 734 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVDRTNKQHSLLCLLMTSCDLSDDT 793
Db 755 YQRMOLDLMDRIILATDLAHLRIFFKDLQKMAEYGVDRTNKQHSLLCLLMTSCDLSDDT 814
QY 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIAMPYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIAMPYKL 874

QY 854 LQDLFPPKAAELYERVASNRHWTQVSHKFTTIRGLPSNNSLDPLDEEYEVPLDGDARAPIN 913
Db 875 LQDLFPPKAAELYERVASNRHWTQVSHKFTTIRGLPSNNSLDPLDEEYEVPLDGDARAPIN 934
QY 914 GCCSLDAE 921
Db 935 GCCSLDAE 942
RESULT 14
US-08-479-532-43
; Sequence 43, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-532-43
Query Match 97.4%; Score 4657; DB 1; Length 942;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 14 QEPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYLLDGSRLVC 73
Db 35 EPPPPQPCADSLQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYLLDGSRLVC 94
QY 74 BEPPHELPOEGKVRRAVTSRKLGCNGLGSPDLPKPLARLVAPLADPTQVLVPLVDKE 133
Db 95 BEPPHELPOEGKVRRAVTSRKLGCNGLGSPDLPKPLARLVAPLADPTQVLVPLVDKE 154
QY 134 AGAAVAATLVHCGQLSDNEEWSLQAVEKHITLVALKRVQALQORESSVAPEATQNPPEAA 193

Db 155 AGAAVAATLVHCGQLSDNEEWSLQAVEKHITLVALKRVQALQORESSVAPEATQNPPEAA 214
QY 194 GDQKGGVAYTNQDRKILQQLCGELYDLDAASSLQKLKVLQYVLOQETQASRCLLLVSDNLQ 253
Db 215 GDQKGGVAYTNQDRKILQQLCGELYDLDAASSLQKLKVLQYVLOQETQASRCLLLVSDNLQ 274
QY 254 SKCVIGDKVLEEEISFPPLTTGRLGQVVEDKKSIOQLKDLTSEDMOQLQSMGCEVQAMLCV 313
Db 275 SKCVIGDKVLEEEISFPPLTTGRLGQVVEDKKSIOQLKDLTSEDMOQLQSMGCEVQAMLCV 334
QY 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTTSLAFQEKQKCEC 373
Db 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTTSLAFQEKQKCEC 394
QY 374 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNABEISVFLDDQNELVAKVDFDGGVDE 433
Db 395 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNABEISVFLDDQNELVAKVDFDGGVDE 454
QY 434 SYEIRIPADOGIAGHVATTGOILNIPDAYAHPFYRGVDDSTGTRTRNLCFPIKNEOE 493
Db 455 SYEIRIPADOGIAGHVATTGOILNIPDAYAHPFYRGVDDSTGTRTRNLCFPIKNEOE 514
QY 494 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSIPEDDTSMALLSMLQDMNFINNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSIPEDDTSMALLSMLQDMNFINNYK 634
QY 614 IDCPTLARFCLMVKKGYRDPYHNWMAFVSVSHCYLLYKNLELTNYLEDMEIFALFTSC 673
Db 635 IDCPTLARFCLMVKKGYRDPYHNWMAFVSVSHCYLLYKNLELTNYLEDMEIFALFTSC 694
QY 674 MCHDLDRGTNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCIFDHSRKD 733
Db 695 MCHDLDRGTNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCIFDHSRKD 754
QY 734 YQRLDLMRDIILATDLAHLRIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQOT 793
Db 755 YQRLDLMRDIILATDLAHLRIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQOT 814
QY 794 KGWKTTRKIAELIYKEFFSQGLEKAMGNRPMWMDREKAYIPELQISFMHIAPIYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGLEKAMGNRPMWMDREKAYIPELQISFMHIAPIYKL 874
QY 854 LQDLFPPKAAELYERVASNRHWTQVSHKFTTIRGLPSNNSLDPLDEEYEVPLDGDARAPIN 913
Db 875 LQDLFPPKAAELYERVASNRHWTQVSHKFTTIRGLPSNNSLDPLDEEYEVPLDGDARAPIN 934
QY 914 GCCSLDAE 921
Db 935 GCCSLDAE 942
RESULT 15
US-08-455-526-43
; Sequence 43, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: US/08/455,526
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/297,494
FILING DATE: 29-AUG-1994
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5789553and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-526-43

Query Match		97.4%;	Score 4657;	DB 1;	Length 942;
Best Local Similarity		98.9%;	Pred. No. 0;	Mismatches 3;	Indels 0; Gaps 0;
Matches 998;		Conservative	7;		
Qy	14	QBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVEALS	AVLPKVTETVTVTL	DGESRLVC	73
Db	35	EPFPPPPQCADSLQDALLSLGSDVIDVAGLQQAQVEALS	AVLPKVTETVTVTL	DGESRLVC	94
Qy	74	EPFPHLPQEGKVRBAVISRKRLGNGLGPSDLPGKPLARL	VAPLAPDTQVLVI	PLVDKE	133
Db	95	EPFPHLPQEGKVRBAVISRKRLGNGLGPSDLPGKPLARL	VAPLAPDTQVLVI	PLVDKE	154
Qy	134	AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQ	ALQOQRESSVAP	EAATONPPEAA	193
Db	155	AGAAVAATLVHCGQLSDNEEWSLQAVEKHTLVALKRVQ	ALQOQRESSVAP	EAATONPPEAA	214
Qy	194	GQKGGVAYTNQDRKITLQCGELYDLDASSLQKVLQYLQ	QETQASRCCLLLV	SDNLQL	253
Db	215	GQKGGVAYTDQDRKITLQCGELYDLDASSLQKVLQYLQ	QETQASRCCLLLV	SDNLQL	274
Qy	254	SCKVIQDKVLEBIEIFPLTTGRLGQVVEDKKSILQKDL	TSEDQMQLQSMG	CEVQAMLCV	313
Db	275	SCKVIQDKVLEBIEIFPLTTGRLGQVVEDKKSILQKDL	TSEDQMQLQSMG	CEVQAMLCV	334
Qy	314	PVISRATQVVALACAFNKLGGDLTDQDEHVIQHC	FHYTSTVL	TSLAFQKEQKLKCEC	373
Db	335	PVISRATQVVALACAFNKLGGDLTDQDEHVIQHC	FHYTSTVL	TSLAFQKEQKLKCEC	394
Qy	374	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICS	VFLDDONELVAK	VDGGVVEDE	433
Db	395	QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICS	VFLDDONELVAK	VDGGVVEDE	454
Qy	434	SYEIRIPADQGIAGHVAITGQILNIPDAYAHP	LFYRGVDDSTG	FRTRNLCFPIKNENQE	493
Db	455	SYEIRIPADQGIAGHVAITGQILNIPDAYAHP	LFYRGVDDSTG	FRTRNLCFPIKNENQE	514
Qy	494	VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAH	SLLYKKVNEAQ	YRSHLANEMMY	553
Db	515	VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAH	SLLYKKVNEAQ	YRSHLANEMMY	574

Qy	554	HMKVSDDYTKLLHDGIQPVAAIDSNFASFTYTPRSL	PEDDTSMAL	SMLQDNFNINNYK	613
Db	575	HMKVSDDYTKLLHDGIQPVAAIDSNFASFTYTPRSL	PEDDTSMAL	SMLQDNFNINNYK	634
Qy	614	IDCPTLARFCLMVKKGYRDPVYHNMHAFSVSHFCYLL	YKNLELTYN	LEDMEIFALFISC	673
Db	635	IDCPTLARFCLMVKKGYRDPVYHNMHAFSVSHFCYLL	YKNLELTYN	LEDMEIFALFISC	694
Qy	674	MCHDLDRHGTNNNSFQVASKSVLAALYSSEGS	VMERHFAQAIAI	LNTHGCNIFDHFSRKD	733
Db	695	MCHDLDRHGTNNNSFQVASKSVLAALYSSEGS	VMERHFAQAIAI	LNTHGCNIFDHFSRKD	754
Qy	734	YQMLDLMRDIILATDLAHLRIIPKDLQMAEVGYD	RNTNKHHSLLL	CLLLMTSCDLSQDT	793
Db	755	YQMLDLMRDIILATDLAHLRIIPKDLQMAEVGYD	RNTNKHHSLLL	CLLLMTSCDLSQDT	814
Qy	794	KGMKTRKIAELIYKEFFSQGDLEKAMGNRPMEM	MDREKAYIPELQIS	FMHEIAMPIYKL	853
Db	815	KGMKTRKIAELIYKEFFSQGDLEKAMGNRPMEM	MDREKAYIPELQIS	FMHEIAMPIYKL	874
Qy	854	LQDLFPKAAELYERVA	SNREHWTKVSHKFTIRGLPSNNSL	DFLDBEYEVPLDGGARAPIN	913
Db	875	LQDLFPKAAELYERVA	SNREHWTKVSHKFTIRGLPSNNSL	DFLDBEYEVPLDGGARAPIN	934
Qy	914	GCCSLDAE	921		
Db	935	GCCSLDAE	942		

Search completed: June 26, 2005, 12:24:02
Job time : 34.1562 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:21:57 ; Search time 114.692 Seconds
(without alignments)
3087.987 Million cell updates/sec

Title: US-10-697-894-39

Perfect score: 4781

Sequence: 1 MRQPAASDLFAQEPVPG.....VPDLGARAPINGCCSLDAS 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	9 US-09-883-825-39	Sequence 39, Appl
2	4781	100.0	921	13 US-10-094-989-5	Sequence 5, Appl
3	4781	100.0	921	16 US-10-697-894-39	Sequence 39, Appl
4	4657	97.4	942	9 US-09-883-825-43	Sequence 43, Appl
5	4657	97.4	942	16 US-10-697-894-43	Sequence 43, Appl
6	4539.5	94.9	920	15 US-10-236-417-78	Sequence 78, Appl
7	4533.5	94.8	920	13 US-10-094-989-2	Sequence 2, Appl
8	4474.5	93.6	941	9 US-09-883-825-45	Sequence 45, Appl
9	4474.5	93.6	941	16 US-10-697-894-45	Sequence 45, Appl
10	4474.5	93.6	941	16 US-10-686-390-5	Sequence 5, Appl
11	4474.5	93.6	941	17 US-10-686-282-5	Sequence 5, Appl

12	4474.5	93.6	941	17 US-10-686-349-5	Sequence 5, Appl
13	4473.5	93.6	905	13 US-10-094-989-4	Sequence 4, Appl
14	4148.5	86.8	950	15 US-10-108-260A-2928	Sequence 2928, Ap
15	3543.5	74.1	786	15 US-10-104-047-2944	Sequence 2944, Ap
16	1766	36.9	334	17 US-10-771-833-30	Sequence 30, Appl
17	1766	36.9	334	17 US-10-886-949-30	Sequence 30, Appl
18	991	20.7	934	9 US-09-891-216-12	Sequence 12, Appl
19	991	20.7	934	9 US-09-891-216-15	Sequence 15, Appl
20	991	20.7	934	14 US-10-168-402-2	Sequence 2, Appl
21	983	20.6	1284	14 US-10-296-144-5	Sequence 5, Appl
22	974.5	20.4	934	14 US-10-168-402-39	Sequence 39, Appl
23	920.5	19.3	684	9 US-09-891-216-14	Sequence 14, Appl
24	920.5	19.3	684	14 US-10-168-402-4	Sequence 4, Appl
25	920.5	19.3	684	16 US-10-746-197-1	Sequence 1, Appl
26	914.5	19.1	779	9 US-09-420-190-1	Sequence 1, Appl
27	914.5	19.1	779	15 US-10-458-839-1	Sequence 6, Appl
28	914.5	19.1	779	15 US-10-440-998-6	Sequence 6, Appl
29	914	19.1	789	9 US-09-321-801-2	Sequence 2, Appl
30	914	19.1	789	15 US-10-618-252-2	Sequence 2, Appl
31	913	19.1	803	15 US-10-440-998-4	Sequence 4, Appl
32	912.5	19.1	766	15 US-10-440-998-2	Sequence 2, Appl
33	912.5	19.1	791	9 US-09-321-801-4	Sequence 4, Appl
34	912.5	19.1	791	15 US-10-618-252-4	Sequence 4, Appl
35	909	19.0	796	9 US-09-321-801-15	Sequence 15, Appl
36	909	19.0	796	15 US-10-618-252-15	Sequence 15, Appl
37	892	18.7	684	14 US-10-168-402-6	Sequence 6, Appl
38	887	18.6	773	14 US-10-202-107-2	Sequence 2, Appl
39	887	18.6	773	17 US-10-887-276-2	Sequence 2, Appl
40	845.5	17.7	576	9 US-09-891-216-13	Sequence 13, Appl
41	845.5	17.7	576	16 US-10-746-197-3	Sequence 3, Appl
42	801	16.8	874	15 US-10-427-222-3	Sequence 3, Appl
43	801	16.8	875	14 US-10-115-515-23	Sequence 23, Appl
44	801	16.8	875	14 US-10-094-168B-5	Sequence 5, Appl
45	801	16.8	875	17 US-10-771-833-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-883-825-39
; Sequence 39, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; Bicknell
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494

481 NILCPPIKNEQVIGVAGLNVKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540
481 NILCPPIKNEQVIGVAGLNVKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540
541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGQPVAAIDSNFASFTYTPRSLPDDTSMALL 600
541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGQPVAAIDSNFASFTYTPRSLPDDTSMALL 600
601 SMLQDMNFNNYKIDCPTLARFCLMVYKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660
601 SMLQDMNFNNYKIDCPTLARFCLMVYKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660
661 LEDMEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
661 LEDMEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
721 HGCNIFDHFSSRKYQRMLDLMDRIILATDLAHLRIFKDLQKMAEYGVDRTNKHSHLL 780
721 HGCNIFDHFSSRKYQRMLDLMDRIILATDLAHLRIFKDLQKMAEYGVDRTNKHSHLL 780
781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELOI 840
781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELOI 840
841 SPWEHIAMPIYKLLQDLFPKAAELYERVAENREHMTKVSHTFTIRGLPSNNSLDFLDEY 900
841 SPWEHIAMPIYKLLQDLFPKAAELYERVAENREHMTKVSHTFTIRGLPSNNSLDFLDEY 900
901 EYVDLDGARAPINGCCSLDAE 921
901 EYVDLDGARAPINGCCSLDAE 921

RESULT 3

US-10-697-894-39
Sequence 39, Application US/10697894
Publication No. US2004012686A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/697,894
FILING DATE: 30-Oct-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/123,783
FILING DATE: 28-July-1998
APPLICATION NUMBER: 08/297,494
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-697-894-39

Query Match 100.0%; Score 4781; DB 16; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRQPAASRDLPFAQBPVPPGSGDGLADALLSLGSLVIVAGLQQAQVKEALSAPLKVETV 60
Db 1 MRRQPAASRDLPFAQBPVPPGSGDGLADALLSLGSLVIVAGLQQAQVKEALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEPPHELPOEGKVRVAVISRKLGCGNLGSPDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEPPHELPOEGKVRVAVISRKLGCGNLGSPDLPGKPLARLVAPLAP 120
QY 121 DTQVLVILPLVDEAGAAVAILVHCGQLSDNEWSLQAVEKHTLVALKVQVQALQOQRESSV 180
Db 121 DTQVLVILPLVDEAGAAVAILVHCGQLSDNEWSLQAVEKHTLVALKVQVQALQOQRESSV 180
QY 181 APEATONPPEAAGDQKGVAYTNQDKILQICGELYDLDASSLQIKVLYQIQOETQASR 240
Db 181 APEATONPPEAAGDQKGVAYTNQDKILQICGELYDLDASSLQIKVLYQIQOETQASR 240
QY 241 CCLLVSEDNQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDEKSTOLKDLTSEDMQQLQ 300
Db 241 CCLLVSEDNQLSCKVIGDKVLEEEISFPLTTGRLGQVVEDEKSTOLKDLTSEDMQQLQ 300
QY 301 SMLGCEVQAMLCVPVISRATDOVALACAFNKGGLDFTDQDEHVIQHFHYTSTVLTST 360
Db 301 SMLGCEVQAMLCVPVISRATDOVALACAFNKGGLDFTDQDEHVIQHFHYTSTVLTST 360
QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEITCSVFLDQNEL 420
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEITCSVFLDQNEL 420
QY 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
QY 481 NILCPPIKNEQVIGVAGLNVKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540
Db 481 NILCPPIKNEQVIGVAGLNVKINGPWFSPKDEDLATAFSYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGQPVAAIDSNFASFTYTPRSLPDDTSMALL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGQPVAAIDSNFASFTYTPRSLPDDTSMALL 600
QY 601 SMLQDMNFNNYKIDCPTLARFCLMVYKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVYKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYNY 660
QY 661 LEDMEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
Db 661 LEDMEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVNERHHFAQAIAINT 720
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Db 721 HGCNIFDHFSSRKYQRMLDLMDRIILATDLAHLRIFKDLQKMAEYGVDRTNKHSHLL 780
QY 781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELOI 840
Db 781 CLMTSCDLSDOTKGWTKTRKIAELIYKEFFSQGLEKAMGNRPMMMDREKAYIPELOI 840

Db 781 CILMTSCDLSQDTGKWKTRTKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQI 840
Qy 841 SFMEHIAPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVPDLGAPINGGCCSLDAE 921
Db 901 EVPDLGAPINGGCCSLDAE 921

RESULT 4

US-09-883-825-43
; Sequence 43, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: No. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 43:

US-09-883-825-43

Query Match 97.4%; Score 4657; DB 9; Length 942;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 14 QEPVPPGGGALQDALLSLGSDIVAGLQAAVKALSAVLPKVETVTVYLLDGSRLVC 73

Db 35 EPPPPPPQCADSLQDALLSLGSDIVAGLQAAVKALSAVLPKVETVTVYLLDGSRLVC 94

Qy 74 BEPPHELPOEGKREAVISRKRLGNGLPGSDLPKPLARLVAPLAPDQTVLVIPLVDKE 133
Db 95 BEPPHELPOEGKREAVISRKRLGNGLPGSDLPKPLARLVAPLAPDQTVLVIPLVDKE 154
Qy 134 AGAVALVILVHCQGLSNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPBAAA 193
Db 155 AGAVALVILVHCQGLSNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPBAAA 214
Qy 194 GDQGGVAYTNODRKILQLCGELYDLDAASSLQVLQYLOQETOASRCCLLVSDNLQOL 253
Db 215 GDQGGVAYTDQDRKILQLCGELYDLDAASSLQVLQYLOQETOASRCCLLVSDNLQOL 274
Qy 254 SKCVIGDKVLEEEISFPLTTGRLQGVVEDKKSIIQLKDLTSDMQOQLQSMGLCEVQAMLCV 313
Db 275 SKCVIGDKVLEEEISFPLTTGRLQGVVEDKKSIIQLKDLTSDMQOQLQSMGLCEVQAMLCV 334
Qy 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAFQKEQKLKCEC 373
Db 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFFHYTSTVLTSTLAFQKEQKLKCEC 394
Qy 374 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGVGVEDE 433
Db 395 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGVGVEDE 454
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFVRGVDSTGFRTRNLCFFPKENQOE 493
Db 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFVRGVDSTGFRTRNLCFFPKENQOE 514
Qy 494 VIGVAELVNKINGPWFPSKFDLATAFSIYCGISIAHSLLYKKNVNAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFPSKFDLATAFSIYCGISIAHSLLYKKNVNAQYRSHLANEMMY 574
Qy 554 HMKYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 613
Db 575 HMKYSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 634
Qy 614 IDCPTLARFCLMWKGYRDPYHNWMAFVSVSHFCYLLYKNLELTNYLEDMEIPALFTSC 673
Db 635 IDCPTLARFCLMWKGYRDPYHNWMAFVSVSHFCYLLYKNLELTNYLEDMEIPALFTSC 694
Qy 674 MCHDLDRGTNNSFOVASKSVLAALYSSEGSVMERHHPAQAIILNTHGCMIFDHFSRKD 733
Db 695 MCHDLDRGTNNSFOVASKSVLAALYSSEGSVMERHHPAQAIILNTHGCMIFDHFSRKD 754
Qy 734 YQRMLDLMRDIIILATDLAHLRIEFDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSDOT 793
Db 755 YQRMLDLMRDIIILATDLAHLRIEFDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSDOT 814
Qy 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQISFMEHIAPIYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQISFMEHIAPIYKL 874
Qy 854 LQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEVEVPDLGAPIN 913
Db 875 LQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEEVEVPDLGAPIN 934
Qy 914 GCCSLDAE 921
Db 935 GCCSLDAE 942

RESULT 5

US-10-697-894-43
; Sequence 43, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.

TITLE OF INVENTION: DNA Encoding Mammalian

Phosphodiesterases

NUMBER OF SEQUENCES: 58

; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-236-417-78									
Query Match 94.9%; Score 4539.5; DB 15; Length 920;									
Best Local Similarity 94.8%; Pred. No. 0;									
Matches 873; Conservative 21; Mismatches 26; Indels 1; Gaps 1;									
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Db	1	MRRQPAASLD	PLAKEP	PGSGDR	DLRDL	DALLSLGS	VIDISGLQ	RAVKEALS	AVLP
Qy	61	YTYLLDGES	RLVCEP	PHQLPQ	EGKVEAV	ISRKRLG	CNGLG	PSDLP	CKPLAR
Db	61	YTYLLDGES	QLVCEP	PHQLPQ	EGKVEAV	ISRKRLG	CNGLG	PSDLP	CKPLAR
Qy	121	DTQVLVPL	VDKEAGA	VAANVIL	VHCGQL	SDNEE	SLQAVE	KHTLV	ALKRVQ
Db	121	DTQVLVPL	ADKEAGA	VAANVIL	VHCGQL	SDNEE	SLQAVE	KHTLV	ALRRVQ
Qy	181	APETQNP	PEAAGD	QKGGV	AYTNQ	DRKILQ	LCGELY	DL	DASSLQ
Db	181	APRAVQN	PPECTA	EDQKGA	AYTDR	DRKILQ	LCGELY	DL	DASSLQ
Qy	241	CCLLLVSE	DNILQ	SKVIGD	KVLGEE	ISFPLT	TGRLG	QV	VEDKKS
Db	241	CCLLLVSE	DNILQ	SKVIGD	KVLGEE	ISFPLT	TGRLG	QV	VEDKKS
Qy	301	SMLGCEV	QAMLC	VPVISR	ATDQ	VVALAC	AFNKL	GGDL	FTD
Db	301	SMLGCEV	QAMLC	VPVISR	ATDQ	VVALAC	AFNKL	GGDL	FTD
Qy	361	LAFQKEQ	KLKCE	QALLQ	VAKNL	FTLH	DDSV	LLQEI	ITEARN
Db	361	LAFQKEQ	KLKCE	QALLQ	VAKNL	FTLH	DDSV	LLQEI	ITEARN
Qy	421	VAKVFDG	GVVDE	SEYETR	IPADQ	GIAG	HVATTG	QILN	IPDAYA
Db	421	VAKVFDG	GVVDE	SEYETR	IPADQ	GIAG	HVATTG	QILN	IPDAYA
Qy	481	NILCFPI	KNEQ	VEIGV	AEVLN	KINGP	WFSK	FDE	LATAFS
Db	481	NILCFPI	KNEQ	VEIGV	AEVLN	KINGP	WFSK	FDE	LATAFS
Qy	541	QYRSHLA	NEMMYH	KVSD	DEYTK	LHDG	IQP	VAAID	SNFAS
Db	541	QYRSHLA	NEMMYH	KVSD	DEYTK	LHDG	IQP	VAAID	SNFAS
Qy	601	SMLODMN	FINNYK	IDCPT	LARF	CLM	VKKGY	RDP	PPYHNM
Db	601	SMLODMN	FINNYK	IDCPT	LARF	CLM	VKKGY	RDP	PPYHNM
Qy	661	LEDMEI	FALF	ISCM	CHDL	HRGT	NNSFQ	VASKS	VLAALY
Db	661	LEDMEI	FALF	ISCM	CHDL	HRGT	NNSFQ	VASKS	VLAALY
Qy	721	HGCNIF	DHFSK	DYQ	RM	DL	MRD	I	LATD
Db	721	HGCNIF	DHFSK	DYQ	RM	DL	MRD	I	LATD
Qy	781	CLLMTS	CDLS	QOT	KGW	TKT	RIAE	LI	YKEP
Db	781	CLLMTS	CDLS	QOT	KGW	TKT	RIAE	LI	YKEP
Qy	841	SFMEHIA	MPYK	LLQ	DL	FPK	AAELY	ERVA	SNRE
Db	841	SFMEHIA	MPYK	LLQ	DL	FPK	AAELY	ERVA	SNRE
Qy	901	EVPLDGA	RAP	ING	CCS	LD	AE		921
Db	901	EVPLDGA	RAP	ING	CCS	LD	AE		920

RESULT 7									
US-10-094-989-2									
; Sequence 2, Application US/10094989									
; Publication No. US20020115179A1									
; GENERAL INFORMATION:									
; APPLICANT: WEI, Ming-Hui et al									
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE									
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN									
; FILE REFERENCE: CL001063DIV									
; CURRENT APPLICATION NUMBER: US/10/094,989									
; CURRENT FILING DATE: 2002-03-12									
; PRIOR APPLICATION NUMBER: 09/754,250									
; NUMBER OF SEQ ID NOS: 5									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 920									
; TYPE: PRT									
; ORGANISM: Homo sapien									
US-10-094-989-2									
Query Match 94.8%; Score 4533.5; DB 13; Length 920;									
Best Local Similarity 94.7%; Pred. No. 0;									
Matches 872; Conservative 21; Mismatches 27; Indels 1; Gaps 1;									
Qy	1	MRRQPAAS	RDLFAQ	EPVP	PGSGDALQ	DALLSLGS	VIDVAGLQ	QAQVKEALS	AVLPK
Db	1	MRRQPAAS	LDPLAK	EPGP	PGSGDR	DLRDL	DALLSLGS	VIDISGLQ	RAVKEALS
Qy	61	YTYLLDGES	RLVCEP	PHQLPQ	EGKVEAV	ISRKRLG	CNGLG	PSDLP	CKPLAR
Db	61	YTYLLDGES	QLVCEP	PHQLPQ	EGKVEAV	ISRKRLG	CNGLG	PSDLP	CKPLAR
Qy	121	DTQVLVPL	VDKEAGA	VAANVIL	VHCGQL	SDNEE	SLQAVE	KHTLV	ALKRVQ
Db	121	DTQVLVPL	ADKEAGA	VAANVIL	VHCGQL	SDNEE	SLQAVE	KHTLV	ALRRVQ
Qy	181	APETQNP	PEAAGD	QKGGV	AYTNQ	DRKILQ	LCGELY	DL	DASSLQ
Db	181	APRAVQN	PPECTA	EDQKGA	AYTDR	DRKILQ	LCGELY	DL	DASSLQ
Qy	241	CCLLLVSE	DNILQ	SKVIGD	KVLGEE	ISFPLT	TGRLG	QV	VEDKKS
Db	241	CCLLLVSE	DNILQ	SKVIGD	KVLGEE	ISFPLT	TGRLG	QV	VEDKKS
Qy	301	SMLGCEV	QAMLC	VPVISR	ATDQ	VVALAC	AFNKL	GGDL	FTD
Db	301	SMLGCEV	QAMLC	VPVISR	ATDQ	VVALAC	AFNKL	GGDL	FTD
Qy	361	LAFQKEQ	KLKCE	QALLQ	VAKNL	FTLH	DDSV	LLQEI	ITEARN
Db	361	LAFQKEQ	KLKCE	QALLQ	VAKNL	FTLH	DDSV	LLQEI	ITEARN
Qy	421	VAKVFDG	GVVDE	SEYETR	IPADQ	GIAG	HVATTG	QILN	IPDAYA
Db	421	VAKVFDG	GVVDE	SEYETR	IPADQ	GIAG	HVATTG	QILN	IPDAYA
Qy	481	NILCFPI	KNEQ	VEIGV	AEVLN	KINGP	WFSK	FDE	LATAFS
Db	481	NILCFPI	KNEQ	VEIGV	AEVLN	KINGP	WFSK	FDE	LATAFS
Qy	541	QYRSHLA	NEMMYH	KVSD	DEYTK	LHDG	IQP	VAAID	SNFAS
Db	541	QYRSHLA	NEMMYH	KVSD	DEYTK	LHDG	IQP	VAAID	SNFAS
Qy	601	SMLODMN	FINNYK	IDCPT	LARF	CLM	VKKGY	RDP	PPYHNM
Db	601	SMLODMN	FINNYK	IDCPT	LARF	CLM	VKKGY	RDP	PPYHNM
Qy	661	LEDMEI	FALF	ISCM	CHDL	HRGT	NNSFQ	VASKS	VLAALY
Db	661	LEDMEI	FALF	ISCM	CHDL	HRGT	NNSFQ	VASKS	VLAALY
Qy	721	HGCNIF	DHFSK	DYQ	RM	DL	MRD	I	LATD
Db	721	HGCNIF	DHFSK	DYQ	RM	DL	MRD	I	LATD
Qy	781	CLLMTS	CDLS	QOT	KGW	TKT	RIAE	LI	YKEP
Db	781	CLLMTS	CDLS	QOT	KGW	TKT	RIAE	LI	YKEP
Qy	841	SFMEHIA	MPYK	LLQ	DL	FPK	AAELY	ERVA	SNRE
Db	841	SFMEHIA	MPYK	LLQ	DL	FPK	AAELY	ERVA	SNRE
Qy	901	EVPLDGA	RAP	ING	CCS	LD	AE		921
Db	901	EVPLDGA	RAP	ING	CCS	LD	AE		920

QY 721 HGCNIEDHFSRKYORMLDMDRIIATDLAHLRIKFKDLOKMAEYGYDRTNKHSHLL 780
Db 720 HGCNIPDFHFSRKYORMLDMDRIIATDLAHLRIKFKDLOKMAEYGYDRTNKHSHLL 779
QY 781 CLIMTSCDLSDOTKGMWTKTKIAELIYKFFSOGDLEKAMGNRPMBMDREKAYIPELQI 840
Db 780 CLIMTSCDLSDOTKGMWTKTKIAELIYKFFSOGDLEKAMGNRPMBMDREKAYIPELQI 839
QY 841 SFMEHIAMPYIKLQDLFPKAAELYERVAASREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 840 SFMEHIAMPYIKLQDLFPKAAELYERVAASREHWTKVSHKFTIRGLPSNNSLDFLDEY 899
QY 901 EYVDLDGARAPINGCCSLDAE 921
Db 900 EYVDLDGTRAPINGCCSLDAE 920

RESULT 8

US-09-883-825-45
; Sequence 45, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-09-883-825-45
Query Match 93.6%; Score 4474.5; DB 9; Length 941;

Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;
QY 14 QBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQKSAVLPKVEIVYVYLLDGSRLVC 73
Db 35 BPVPPQCADSLQDALLSLGSDVIDISGLQRAKSAVLPKVEIVYVYLLDGSRLVC 94
QY 74 BEPPHELPOEGKREAVISRKRLGNGLGSPSLPKPKLARLVAPLADPTQVILVPIVDKE 133
Db 95 EDPPELPOEGKREAVISRKRLGNGLGSPSLPKPKLARLVAPLADPTQVILVPIVDKE 154
QY 134 AGAAVAIVLHCGQLSDNEESLQAEVHTLVAKVQNALQOQRESSVAPEATONPEEAA 193
Db 155 AGAAVAIVLHCGQLSDNEESLQAEVHTLVAKVQNALQOQRESSVAPEATONPEEAA 214
QY 194 GDQGGVAYTNDRIKILQCGELYDLDAASSLQKLVQLVQLQOQETASRCCLLLVSEDLQ 253
Db 215 EDQGGVAYTNDRIKILQCGELYDLDAASSLQKLVQLVQLQOQETASRCCLLLVSEDLQ 274
QY 254 SKVIGDKVLBEERISFPLTTGRLGQVVEDKKSILKDLTSDMQQLQSMGCEVQAMLCV 313
Db 275 SKVIGDKVLBEERISFPLTTGRLGQVVEDKKSILKDLTSDMQQLQSMGCEVQAMLCV 333
QY 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQEKQKCEC 373
Db 334 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSTLAFQEKQKCEC 393
QY 374 QALQVAKNLTFLHDDVSVLQEIITEARNLSNABICSVFLDDONELVAKVDFGGVDE 433
Db 394 QALQVAKNLTFLHDDVSVLQEIITEARNLSNABICSVFLDDONELVAKVDFGGVDE 453
QY 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHLFVRGVDDSTGFRTRNLCFPIKNEQ 493
Db 454 SYEIRIPADQGIAGHVATTGQILNIPDAYAHLFVRGVDDSTGFRTRNLCFPIKNEQ 513
QY 494 VIGVAELVKNKINGPWFSGFDEDLATAFSIYCGISIAHSLLYKKNVQAEQVRSHLANEMMY 553
Db 514 VIGVAELVKNKINGPWFSGFDEDLATAFSIYCGISIAHSLLYKKNVQAEQVRSHLANEMMY 573
QY 554 HMKVSDDEYTKLLHDGIOPVAAIDSNPASFTVTPSLPDDTSMALSLQDMNFINNYK 613
Db 574 HMKVSDDEYTKLLHDGIOPVAAIDSNPASFTVTPSLPDDTSMALSLQDMNFINNYK 633
QY 614 IDCPTLARFCLMVKKGYRDPYHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 673
Db 634 IDCPTLARFCLMVKKGYRDPYHNMMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFISC 693
QY 674 MCHDLHRGTNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 733
Db 694 MCHDLHRGTNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHFSRKD 753
QY 734 YORMLDLMDRIIATDLAHLRIKFKDLOKMAEYGYDRTNKHSHLLCLMTSCDLSDOT 793
Db 754 YORMLDLMDRIIATDLAHLRIKFKDLOKMAEYGYDRTNKHSHLLCLMTSCDLSDOT 813
QY 794 KGWTKTKIAELIYKFFSOGDLEKAMGNRPMBMDREKAYIPELQISFMEHIAMPYIKL 853
Db 814 KGWTKTKIAELIYKFFSOGDLEKAMGNRPMBMDREKAYIPELQISFMEHIAMPYIKL 873
QY 854 LQDLFPKAAELYERVAASREHWTKVSHKFTIRGLPSNNSLDFLDEEYVDPDGDARAPIN 913
Db 874 LQDLFPKAAELYERVAASREHWTKVSHKFTIRGLPSNNSLDFLDEEYVDPDGDARAPIN 933
QY 914 GCCSLDAE 921
Db 934 GCCSLDAE 941

RESULT 9
US-10-697-894-45
; Sequence 45, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:


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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-390-5

Query Match      93.6%; Score 4474.5; DB 16; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QBPVPGSGDALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYLLDGSRLVC 73
DB 35 EPPPPQPCADSLQDALLSLGSDVIDISGLQRAVKEALSAPRVETVYTYLLDGSQVC 94
QY 74 EPPHELPOEGKREAVISRKRLGCGNGLGFSGLPGKPLARLVAPLAPDTQVLPVLDKE 133
DB 95 EPPHELPOEGKREAVISRKRLGCGNGLGFSGLPGKPLARLVAPLAPDTQVLPVLDKE 154
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 193
DB 155 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQVQLQGRPREAPRAVQNPPEGTA 214
QY 194 GQKGGVAVTNDKRLQLCGELYDLDAASLQKVLQYLOQETQASRCCLLLVSEDNLQL 253
DB 215 EDQKGGAAVTDKRLQLCGELYDLDAASLQKVLQYLOQETQASRCCLLLVSEDNLQL 274
QY 254 SKCVIGDKVLEBESIPPLTGRGQVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 313
DB 275 SKCVIGDKVLEBESVPL-TGCLGQVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 333
QY 314 PVISRATQDQVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSLTAFQEKQLKCB 373
DB 334 PVISRATQDQVALACAFNKLGGDLFTDQDEHVIQHCFTYTSVLTSLTAFQEKQLKCB 393
QY 374 QALLQVAKNLFTHLDVSVLLQEIITEARNLNAEICSVFLLDQNELVAKVDFGQVDE 433
DB 394 QALLQVAKNLFTHLDVSVLLQEIITEARNLNAEICSVFLLDQNELVAKVDFGQVDE 453
QY 434 SYEIRIPADQGIAGHVATTGQILNTPDAYAHPLFYRGVDDSTGFRNLTCPPIKNQOE 493
DB 454 SYEIRIPADQGIAGHVATTGQILNTPDAYAHPLFYRGVDDSTGFRNLTCPPIKNQOE 513
QY 494 VIGVAELVNKINGPFSKPEDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
DB 514 VIGVAELVNKINGPFSKPEDLATAFSYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573
QY 554 HMKVSDDEVTKLHDGQIPVAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 613
DB 574 HMKVSDDEVTKLHDGQIPVAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYK 633
QY 614 IDCPTLARCLMVKGYRPPPHNNWHAESVSHFCYLLLYKNELTYLNEYDMEIFALFISC 673
DB 634 IDCPTLARCLMVKGYRPPPHNNWHAESVSHFCYLLLYKNELTYLNEYDMEIFALFISC 693
QY 674 MCHDLDRGTNNNSFOVAKSVLAALYSSEGSVNERHHFAQATAILNTHGCNIFDHFSRKD 733
DB 694 MCHDLDRGTNNNSFOVAKSVLAALYSSEGSVNERHHFAQATAILNTHGCNIFDHFSRKD 753
QY 734 YQRMLDLMDRIIATDLAHLRI FKDLQKQVAVGVYDRTNKQHSLLLCLLMTSCDLSQDT 793
DB 754 YQRMLDLMDRIIATDLAHLRI FKDLQKQVAVGVYDRTNKQHSLLLCLLMTSCDLSQDT 813
QY 794 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIANPIYKL 853
DB 814 KGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMDREKAYIPELQISFMEHIANPIYKL 873
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QY 854 LODLPKAAELYERVASNRHWTKVSHKFTIRGLPNNNSLDPLDEBYEVPDLQGAAPIN 913
DB 874 LODLPKAAELYERVASNRHWTKVSHKFTIRGLPNNNSLDPLDEBYEVPDLQGAAPIN 933
QY 914 GCCLSDAE 921
DB 934 GCCLSDAE 941

RESULT 11
US-10-686-282-5
; Sequence 5, Application US/10686282
; Publication No. US20050020547A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343D
; CURRENT APPLICATION NUMBER: US/10/686,282
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-282-5

Query Match      93.6%; Score 4474.5; DB 17; Length 941;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QBPVPGSGDALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVTYTYTYLLDGSRLVC 73
DB 35 EPPPPQPCADSLQDALLSLGSDVIDISGLQRAVKEALSAPRVETVYTYTYLLDGSQVC 94
QY 74 EPPHELPOEGKREAVISRKRLGCGNGLGFSGLPGKPLARLVAPLAPDTQVLPVLDKE 133
DB 95 EPPHELPOEGKREAVISRKRLGCGNGLGFSGLPGKPLARLVAPLAPDTQVLPVLDKE 154
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPEATQNPPEAA 193
DB 155 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQVQLQGRPREAPRAVQNPPEGTA 214
QY 194 GQKGGVAVTNDKRLQLCGELYDLDAASLQKVLQYLOQETQASRCCLLLVSEDNLQL 253
DB 215 EDQKGGAAVTDKRLQLCGELYDLDAASLQKVLQYLOQETQASRCCLLLVSEDNLQL 274
QY 254 SKCVIGDKVLEBESIPPLTGRGQVVEDKKSITQLKDLTSEDQQQLQSMGCEVQAMLCV 313
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[illegible]

RESULT 12

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RES001.12
US-10-686-349-5
; Sequence 5, Application US/10686349
; Publication No. US20050070499A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343C
; CURRENT APPLICATION NUMBER: US/10/686,349
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05

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; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-349-5

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Query Match	93.6%	Score 4474.5	DB 17	Length 941
Best Local Similarity	94.7%	Pred. No. 0		
Matches 860	Conservative 21	Mismatches 26	Indels 1	Gaps 1
Qy	14	QEPVPPSGDGLQDALLSGVSDIVAGLQQAKEALSAVLPKVETVYTVLLDGESRLVC	73	
Db	35	EPPPPQPCADSLQDALLSGVSDISGLQRAKEALSAVLPKVETVYTVLLDGESQLVC	94	
Qy	74	EBPPHELPOBQGVKREAVISKRKRLGCGNLGSPDLPGKPLARLAVLAPLAPDTQVLVPLVDKE	133	
Db	95	EDPPHELPOBQGVKREAIISQKRLGCGNLGSPDLPGKPLARLAVLAPLAPDTQVLVPLADKE	154	
Qy	134	AGAAVAVILVHCQLSDNEBWSLOAVEKHITLVALKRVQALQOBRESSVAEATONPBEAA	193	
Db	155	AGAAVAVILVHCQLSDNEBWSLOAVEKHITLVALRVRVQLVQORGPPEAPRAVQPEGTA	214	
Qy	194	GDQGGVAYTNDRKILQLCGELYDLIDASSLQKLVLQYLQOETOASRCCLLLVSENLQL	253	
Db	215	EDQGGNAYTDRKILQLCGELYDLIDASSLQKLVLQYLQOETRASRCCLLLVSENLQL	274	
Qy	254	SKVIGDKVLJEBISFPLTTGRLGQGVVEDKKSIOQLKDLTSEDQQQLSMGLGCEVQAMLCV	313	
Db	275	SKVIGDKVLJEBVSFPL-TGCLGQGVVEDKKSIOQLKDLTSEDVQQLSMGLGCELQAMLCV	333	
Qy	314	PVLSRATDQVVALACAFNKLGGDLFTDDEHVTLOHCFHYTSTVLTSTLAFQKEOKLKCEC	373	
Db	334	PVLSRATDQVVALACAFNKLGGDLFTDDEHVTLOHCFHYTSTVLTSTLAFQKEOKLKCEC	393	
Qy	374	QALLQVAKNLFTHLDDVSVLLQBIITEARNLSNABICSVFLDQNELVAKVFDGGVVDE	433	
Db	394	QALLQVAKNLFTHLDDVSVLLQBIITEARNLSNABICSVFLDQNELVAKVFDGGVVDE	453	
Qy	434	SYEIRPADQGIAGHVATTQIILNIPDAVAHPULFYRGVDDSTGFRTRNLCPPIKNENQE	493	
Db	454	SYEIRPADQGIAGHVATTQIILNIPDAVAHPULFYRGVDDSTGFRTRNLCPPIKNENQE	513	
Qy	494	VIGVAELVNKINGPWFSEKDEDATAFSYICGSIASHSLLYKKVNAQYRSHLANEMMY	553	
Db	514	VIGVAELVNKINGPWFSEKDEDATAFSYICGSIASHSLLYKKVNAQYRSHLANEMMY	573	
Qy	554	HMKVSDEYTKLHDGIQPVAADSNFASFTYTPRSLPEDDTSMALLSMQDNFNINNYK	613	
Db	574	HMKVSDEYTKLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMQDNFNINNYK	633	
Qy	614	IDCPTLARFCMLVKKGYRDPYPYNNWMAFSVSHFCYLLLYKNLELTNYLEDMEITFALFISC	673	
Db	634	IDCPTLARFCMLVKKGYRDPYPYNNWMAFSVSHFCYLLLYKNLELTNYLEDIEITFALFISC	693	
Qy	674	MCDDLHRGTNNSFQVASKSVLAALYSSSGSVMERHFAQATAILNTHGCNIFDHFSRKD	733	
Db	694	MCDDLHRGTNNSFQVASKSVLAALYSSSGSVMERHFAQATAILNTHGCNIFDHFSRKD	753	
Qy	734	YQRLMLDMRDIILATDLAHLRLFKDLQKMAEYGYDRTNKHSHSLLLCLLMTSCDLSDOT	793	
Db	754	YQRLMLDMRDIILATDLAHLRLFKDLQKMAEYGYDRTNKHSHSLLLCLLMTSCDLSDOT	813	


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QY 794 KGWTKRTRKIAELIYKEFFSQGDLEKAMGNRPMMMDREKAYIPBLOISFMEHIAMPIYKL 853
DB 814 KGWTKRTRKIAELIYKEFFSQGDLEKAMGNRPMMMDREKAYIPBLOISFMEHIAMPIYKL 873
QY 854 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEBEYVDPDLGGRAPIN 913
DB 874 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEBEYVDPDLGGRAPIN 933
QY 914 GCCSLDAE 921
DB 934 GCCSLDAE 941

RESULT 13
US-10-094-989-4
; Sequence 4, Application US/10094989
; Publication No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 905
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-989-4

Query Match 93.6%; Score 4473.5; DB 13; Length 905;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 860; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

QY 16 PVPPGSGDGLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTYVTVYLLDGSRLVCE 75
DB 1 PPPPQPCADSLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTYVTVYLLDGSRLVCE 60
QY 76 PPHELPOEGKVRKREAVISRKRKLCNGSLGSLVDVAGLQAVKEALSAPDQVLPVLDKQAG 135
DB 61 PPHELPOEGKVRKREAVISRKRKLCNGSLGSLVDVAGLQAVKEALSAPDQVLPVLDKQAG 120
QY 136 AVAAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPENATQNPPEAAGD 195
DB 121 AVAAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPENATQNPPEAAGD 180
QY 196 QKGGVAYTNODRKILQLCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSEDLNLQSC 255
DB 181 QKGGAAAYTDRDKILQLCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSEDLNLQSC 240
QY 256 KVIGDKVLEEEISFPPLTTGRLGQVVEDKKSIIQLKDLTSEDQMQLQSMGLGCEVQAMLCVPV 315
DB 241 KVIGDKVLEEEISFPPL-TGCLGQVVEDKKSIIQLKDLTSEDVQQLQSMGLGCEVQAMLCVPV 299
QY 316 ISRATDQVVALACAFNKLGGLDFTDQDEHVIQHCFTHTSTVLTSTIAFQKQKLCCEQA 375
DB 300 ISRATDQVVALACAFNKLEGLDFTDEDEHVIQHCFTHTSTVLTSTIAFQKQKLCCEQA 359
QY 376 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVPFLDQNELVAKVFDGCVVEDSEY 435
DB 360 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNABI CSVPFLDQNELVAKVFDGCVVEDSEY 419
QY 436 EIRIPADQGIAGHVAATTGQILNI PAYAHPLEFYRGVDDSTGFRTRNIIICFPFKENQEVY 495
DB 420 EIRIPADQGIAGHVAATTGQILNI PAYAHPLEFYRGVDDSTGFRTRNIIICFPFKENQEVY 479
QY 496 GVAELVNKINGPWFPSKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHM 555
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DB 480 GVAELVNKINGPWFPSKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHM 539
QY 556 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMQDMNFNNYKID 615
DB 540 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMQDMNFNNYKID 599
QY 616 CPTLARFCLMWKGGYRDPYPHNMMHAFSVSHFCYLLYKQLELTNYLEDMEIIPALFISCMC 675
DB 600 CPTLARFCLMWKGGYRDPYPHNMMHAFSVSHFCYLLYKQLELTNYLEDIEIPALFISCMC 659
QY 676 HOLDRGTNNNSFOVASKSVLAALYSSEGSVMRHHFAQAIAIINTHGNCIFOHFSRKYQ 735
DB 660 HOLDRGTNNNSFOVASKSVLAALYSSEGSVMRHHFAQAIAIINTHGNCIFOHFSRKYQ 719
QY 736 RMLDLWRDIIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQTKG 795
DB 720 RMLDLWRDIIILATDLAHLRIFKDLQKMAEVGYDRTNKHSHLLCLLMTSCDLSQTKG 779
QY 796 WKTTRKIAELIYKEFFSQGDLEKAMGNRPMMMDREKAYIPBLOISFMEHIAMPIYKLQ 855
DB 780 WKTTRKIAELIYKEFFSQGDLEKAMGNRPMMMDREKAYIPBLOISFMEHIAMPIYKLQ 839
QY 856 DLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDBEYVDPDLGGRAPINGC 915
DB 840 DLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDBEYVDPDLGGRAPINGC 899
QY 916 CSLDAE 921
DB 900 CSLDAE 905

RESULT 14
US-10-108-260A-2928
; Sequence 2928, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2928
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2928

Query Match 86.8%; Score 4148.5; DB 15; Length 950;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 800; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QSPVPPGSGDGLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTYVTVYLLDGSRLVYC 73
DB 104 PPPPPQPCADSLQDALLSLGSLVDVAGLQAVKEALSAVLPKVTYVTVYLLDGSRLVYC 163
QY 74 BEPPHELPOEGKVRKREAVISRKRKLCNGSLGSLVDVAGLQAVKEALSAPDQVLPVLDKQ 133
DB 164 BEPPHELPOEGKVRKREAVISRKRKLCNGSLGSLVDVAGLQAVKEALSAPDQVLPVLDKQ 223
QY 134 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPENATQNPPEAA 193
DB 224 AGAAVAVILVHCGQLSDNEEWSLQAVKHTLVALKRVQALQOQRESSVAPENATQNPPEAA 283
QY 194 GDQKGGVAYTNODRKILQLCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSEDLNLQ 253
DB 284 EDQKGGAAAYTDRDKILQLCGELYDLDAASSLQKVLQYLOQETQASRCCLLLVSEDLNLQ 343
QY 254 SKCVIGDKVLEEEISFPPLTTGRLGQVVEDKKSIIQLKDLTSEDQMQLQSMGLGCEVQAMLCV 313
DB 344 SKCVIGDKVLEEEISFPPL-TGCLGQVVEDKKSIIQLKDLTSEDVQQLQSMGLGCEVQAMLCV 402
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314	Qy	PVISRATQVVALLACAFNKLGGDLPTDQDEHVHQCHFHYTSTVLSTLFAQEQKQKCBEC	373
403	Db	PVISRATQVVALLACAFNKLGGDLPTDQDEHVHQCHFHYTSTVLSTLFAQEQKQKCBEC	462
374	Qy	QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDE	433
463	Db	QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDE	522
434	Qy	SYEIRIPADQGIAGHVAITGQILNIPDAYAHPLFYRGVDDSGTFRNLCFPIKNENQE	493
523	Db	SYEIRIPADQGIAGHVAITGQILNIPDAYAHPLFYRGVDDSGTFRNLCFPIKNENQE	582
494	Qy	VIGVAELVNKINGPWFSPFDEDLATAFSYICISIAHSLLYKKVNEAQYRSHLANEMMY	553
583	Db	VIGVAELVNKINGPWFSPFDEDLATAFSYICISIAHSLLYKKVNEAQYRSHLANEMMY	642
554	Qy	HMKYSDBEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK	613
643	Db	HMKYSDBEYTKLLHDGIPQVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK	702
614	Qy	IDCPTLARFCLMVKKGYRDPYPVHNMMHAFSVSHFCYLLYKNLENTLYLDEMEIFALFISC	673
703	Db	IDCPTLARFCLMVKKGYRDPYPVHNMMHAFSVSHFCYLLYKNLENTLYLDEMEIFALFISC	762
674	Qy	MCHDLDRHGTNNSFQVASKSVLAALYSSEGVSVERHHFPAQAIATLNTHGCI1FDHFSRKD	733
763	Db	MCHDLDRHGTNNSFQVASKSVLAALYSSEGVSVERHHFPAQAIATLNTHGCI1FDHFSRKD	822
734	Qy	YQRMLDLWRDIIILATDLAHLURI1FKDLQMAEYGYDRTNKQHSILLCILMTSCDLSQDT	793
823	Db	YQRMLDLWRDIIILATDLAHLURI1FKDLQMAEYGYDRNNKQHRLULCLLMTSCDLSQDT	882
794	Qy	KGWKTTRKIAELI1YKEPFSQGDLEKAMGNRPWEMMDREKAYIPELQISFMEHIAMPIYKL	853
883	Db	KGWKTTRKIAELI1YKEPFSQGDLEKAMGNRPWEMMDREKAYIPELQISFMEHIAMPIYKL	942
854	Qy	LQDLFFPKA 861	
943	Db	LQDLFFPLA 950	

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RESULT 15
US-10-104-047-2944
; Sequence 2944, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2944
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2944

```

Query Match	74.1%;	Score 3543.5;	DB 15;	Length 786;
Best Local Similarity	93.8%;	Pred. No. 5.1e-289;		
Matches 684;	Conservative 21;	Mismatches 23;	Indels 1;	Gaps 1;

Qy	1	MRRQPAASRLDFAQEPVP	PGSGD	GALQD	ALLSLG	SVSD	IVAGLQ	QAQV	KEALSA	VLPKV	ETV	60
			:		:		:		:		:	
Db	1	MRRQPAASLDPLAKEP	PGPGSR	DRLED	ALLSLG	SVSD	ISGLQ	RAVKEAL	SAVLPR	VETV		60
			:		:		:		:		:	
Qy	61	YTVLLDGESRLVCEEP	PHPEL	POEGKV	TEAVI	SRKRLG	CNGL	GFSD	LPGKPL	ARLVA	PLAP	120
			:		:		:		:		:	
Db	61	YTVLLDGESQLVCDD	PHPEL	POEGKV	TEAII	SRKRLG	CNGL	GFSD	LPGKPL	ARLVA	PLAP	120
			:		:		:		:		:	

Qy	121	DTQVLVITPLVDKEAGAAVAATILVHCQGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV	180
Db	121	DTQVLVNPPLADKEAGAAVAATILVHCQGQLSDNEEWSLQAVEKHTLVALRVRQVQLQGRPRE	180
Qy	181	APEATONPPREAAAGDQGGVAYTNQDRKILQCCELYDLDDASSLQKVLQVLYQQEQTASR	240
Db	181	APRAVQNPPEGTABDQGGAAAYTDRDRKILQCCELYDLDDASSLQKVLQVLYQQEQTASR	240
Qy	241	CCLLLVSEDNILQLSCVKYIGDKVLEEEESFPPTTGRGLQGVQVEDKKSQIKLDLTSEDWQQQLQ	300
Db	241	CCLLLVSEDNILQLSCVKYIGDKVLEEVSFPL-TGCLQGVQVEDKKSQIKLDLTSEDVQQQLQ	299
Qy	301	SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLTST	360
Db	300	SMLGCELQAMLCVPVISRATDQVVALACAFNKLGGDLFTDEDEHVIQHCFTYSTVLTST	359
Qy	361	LAFQEKQLKCECQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL	420
Db	360	LAFQEKQLKCECQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL	419
Qy	421	VAKVFDGGVVEDSEYEIRIPADQGIAGHVAATTGQILNIPDAYAHPLFYRGVDDSTGFRTR	480
Db	420	VAKVFDGGVVDSEYEIRIPADQGIAGHVAATTGQILNIPDAYAHPLFYRGVDDSTGFRTR	479
Qy	481	NILCFPIKNEQNOEVIQVABLUNKINGPWFSEFDEDLATAFSYCGISTAHSLLYKKVNEA	540
Db	480	NILCFPIKNEQNOEVIQVABLUNKINGPWFSEFDEDLATAFSYCGISTAHSLLYKKVNEA	539
Qy	541	QYRSHLANEMMYHMKYSDDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPDDDTSMALL	600
Db	540	QYRSHLANEMMYHMKYSDDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPDDDTSMALL	599
Qy	601	SMLODMNFINNYKIDCPTLARFCMLVKGYRDPDPYHNMMHAFSVSHFCVLLYKNLELTNY	660
Db	600	SMLODMNFINNYKIDCPTLARFCMLVKGYRDPDPYHNMMHAFSVSHFCVLLYKNLELTNY	659
Qy	661	LEDMIEIPALFISCMCHDLDRHTGWNNSFCVASKSVLAALYSEGSVWERHHFAQATAILNT	720
Db	660	LEDIEIPALFISCMCHDLDRHTGWNNSFCVASKSVLAALYSEGSVWERHHFAQATAILNT	719
Qy	721	HGCNIPDHF 729	
Db	720	HGCNIPDHF 728	

Search completed: June 26, 2005, 12:40:58
Job time : 118.692 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:11 ; Search time 115.187 Seconds
(without alignments)
3092.423 Million cell updates/sec

Title: US-10-697-894-39
Perfect score: 4781
Sequence: 1 MRQPAASRDLFQAEVPRG.....VPDLGARAPINGCCSLDAE 921

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4781	100.0	921	2 AAR69727	Cyclic-GMP
2	4781	100.0	921	2 AAW11252	Clone p3C
3	4781	100.0	921	2 AAW18048	Cyclic-GMP
4	4781	100.0	921	2 AAW71224	CGS-PDE e
5	4781	100.0	921	2 AAW77040	Adrenal c
6	4781	100.0	921	2 AAW60752	CGS-PDE i
7	4781	100.0	921	3 AAY80984	Bovine ad
8	4781	100.0	921	6 ABUS8723	Bovine ad
9	4781	100.0	921	8 ADQ94959	Bovine p3
10	4764	99.6	921	2 AAR28407	CGS-PDE f
11	4657	97.4	942	2 AAR69728	Cyclic-GMP
12	4657	97.4	942	2 AAW11239	Cyclic-GMP
13	4657	97.4	942	2 AAW18049	CGS-PDE a
14	4657	97.4	942	2 AAW71225	Bovine br
15	4657	97.4	942	2 AAW77041	Cyclic-GMP
16	4657	97.4	942	2 AAW60753	CGS-PDE i
17	4657	97.4	942	3 AAY80985	Bovine br
18	4657	97.4	942	6 ABUS8724	Bovine br
19	4657	97.4	942	8 ADQ94963	Bovine CG
20	4617	96.6	942	2 AAR28408	CGS-PDE f
21	4539.5	94.9	920	6 ABR54205	Human NOV
22	4533.5	94.8	920	5 AAO15507	Human NOV
23	4533.5	94.8	920	5 ABG70998	Human pho
24	4474.5	93.6	941	2 AAR69729	Cyclic-GMP
25	4474.5	93.6	941	2 AAW11253	pHCGs6n c

26	4474.5	93.6	941	2 AAW18050	Human CGS
27	4474.5	93.6	941	2 AAW71226	Human CGS
28	4474.5	93.6	941	2 AAW77042	Cyclic-GMP
29	4474.5	93.6	941	2 AAW60754	Human CGS
30	4474.5	93.6	941	3 AAY80986	Human CGS
31	4474.5	93.6	941	4 AAS07954	Human pho
32	4474.5	93.6	941	4 AAE07918	Human pho
33	4474.5	93.6	941	4 AAB85117	Human CGM
34	4474.5	93.6	941	4 AAB85106	Human CGM
35	4474.5	93.6	941	4 AAG66539	Human int
36	4474.5	93.6	941	6 ABUS8725	Human bra
37	4474.5	93.6	941	7 ADD14154	Human bra
38	4474.5	93.6	941	7 ADE62314	Human pro
39	4474.5	93.6	941	8 ADO21792	Human pho
40	4474.5	93.6	941	8 ADQ94965	Plasmid p
41	4436.5	92.8	941	2 AAR28409	Human foe
42	4324.5	90.5	928	7 ADE62312	Rat Prote
43	4148.5	86.8	950	7 ADM04243	Human pro
44	3543.5	74.1	786	7 ADB64790	Human pro
45	3229	67.5	685	8 ADR10446	Human pro

ALIGNMENTS

RESULT 1

AAR69727

ID AAR69727 standard; protein; 921 AA.

AC AAR69727;

XX

XX

DT 25-MAR-2003 (revised)

DT 11-OCT-1995 (first entry)

XX

XX

DE Cyclic-GMP stimulated nucleotide PDE clone p3CGS-5.

XX

KW Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies;

KW bovine adrenal cortex; hormones; neurotransmitters;

KW transmission regulation; enzyme purification; clone p3CGS-5.

XX

OS Bos taurus.

XX

PN US5389527-A.

XX

PD 14-FEB-1995.

XX

PF 20-APR-1992; 92US-00872644.

XX

PR 19-APR-1991; 91US-00688356.

XX

PA (UNIW) UNIV WASHINGTON.

XX

XX

PI Sonnenburg WK, Charbonneau H, Beavo JA;

XX

WPI; 1995-090205/12.

XX

N-PSDB; AAQ83974.

XX

PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-

diesterase - and related vectors and transformed cells, useful for

screening cpds. for phospho-di:esterase modulating activity.

XX

PS Claim 1; Col 65-74; 69pp; English.

XX

CC AAQ83974 encodes AAR69727 the bovine adrenal cortex cyclic-GMP stimulated

nucleotide phospho-diesterase (Cam PDE) clone p3CGS-5. Eukaryotic cells

that express Cam PDE can be used to screen cpds. for the ability to

modulate Cam PDE activity. Cam PDEs are involved in regulating the

transmission of information from hormones, neurotransmitters or other

systems that use cyclic nucleotides as messengers. Antibodies raised

against Cam PDE can be used for enzyme purificn., or determination.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX

Sequence 921 AA;

```
Query Match      100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRQPAASRDLPFAQBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
DB 1 MRRQPAASRDLPFAQBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKLGCNGLGSPDLPGKPLARLAP 120
DB 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKLGCNGLGSPDLPGKPLARLAP 120
QY 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQRESSV 180
DB 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQRESSV 180
QY 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQCGELYDLDASSLQKVLQYLQQTQASR 240
DB 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQCGELYDLDASSLQKVLQYLQQTQASR 240
QY 241 CCLLVSDNLQSKVIGDKVLEBIEISFPLTTGRLGQVVEDKGIQKDLTSEDMQQLQ 300
DB 241 CCLLVSDNLQSKVIGDKVLEBIEISFPLTTGRLGQVVEDKGIQKDLTSEDMQQLQ 300
QY 301 SMLGCEVQAMLCVPISRATDOVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLST 360
DB 301 SMLGCEVQAMLCVPISRATDOVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLST 360
QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLDQNEL 420
DB 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNABICSVFLDQNEL 420
QY 421 VAKVPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDTGFTR 480
DB 421 VAKVPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDTGFTR 480
QY 481 NILCPPIKNEQEVIGVLAELVKNKNGPWFSEDEDLATAFSTYCGISIAHSLLYKKVNEA 540
DB 481 NILCPPIKNEQEVIGVLAELVKNKNGPWFSEDEDLATAFSTYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGICQVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
DB 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGICQVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
QY 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPHNNWHAFSVSHFCYLLYKNLELTYN 660
DB 601 SMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYPHNNWHAFSVSHFCYLLYKNLELTYN 660
QY 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHFAQATAILNT 720
DB 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHFAQATAILNT 720
QY 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHHSLLL 780
DB 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHHSLLL 780
QY 781 CLMTSCDLSQDTKGWTKTRKIAELIYKEFPQGDLEKAMGNRPNMMDREKAYIPELQI 840
DB 781 CLMTSCDLSQDTKGWTKTRKIAELIYKEFPQGDLEKAMGNRPNMMDREKAYIPELQI 840
QY 841 SFMEHIANPIYKLLQDLFPKAAELYERVAENREHTKVSHTKFTIRGLPSNNSLDLDEY 900
DB 841 SFMEHIANPIYKLLQDLFPKAAELYERVAENREHTKVSHTKFTIRGLPSNNSLDLDEY 900
QY 901 EVPDLGAPINGCCSILDAE 921
DB 901 EVPDLGAPINGCCSILDAE 921
```

RESULT 2
AAW11252

ID AAW11252 standard; protein; 921 AA.

```
XX AC AAW11252;
XX 25-MAR-2003 (revised)
XX 17-MAR-1997 (first entry)
XX Clone p3CGS-5 cyclic GMP stimulated phosphodiesterase.
XX Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; CAMP;
XX adrenal gland; cGMP; transmembrane signal; extracellular hormone;
XX neurotransmitter; antibody.
XX Bos taurus.
XX US5580771-A.
XX 03-DEC-1996.
XX 29-AUG-1994; 94US-00297494.
XX 19-APR-1991; 91US-00688356.
XX 20-APR-1992; 92US-00872644.
XX (UNITW ) UNIV WASHINGTON.
XX Charbonneau H, Sonnenburg WK, Beavo JA;
XX WPI; 1997-033573/03.
XX N-PSDB; AAT51110.
XX DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
XX recombinant enzyme.
XX Example 4; Col 65-72; 68pp; English.
XX This sequence represents the cyclic GMP stimulated phosphodiesterase (cGS
XX -PDE) clone p3CGS-5 isolated from bovine adrenal cortex. The cyclic
XX nucleotide phosphodiesterases (PDEs) catalyze the hydrolysis of 3', 5'
XX cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'-
XX nucleotide monophosphates. The PDEs are therefore important in the
XX control of the cellular concentration of cyclic nucleotides. The PDEs
XX are, in turn, regulated by transmembrane signals or second messenger
XX ligands such as calcium ion or cGMP. The PDEs therefore have a central
XX role in regulating the flow of information from extracellular hormones,
XX neurotransmitters, or other signals that use the cyclic nucleotides as
XX messengers. PDEs are present in most of the cells and tissues of
XX eukaryotic organisms, but only in trace amounts. cGS-PDEs are stimulated
XX by cGMP in effecting cAMP hydrolysis. This is thought to occur through a
XX noncatalytic cGMP-specific site present on the cGS-PDE. The cDNA encoding
XX this sequence can be used for the production of recombinant cGS-PDE.
XX which may have therapeutic and diagnostic uses. This protein may also be
XX useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
XX correct PF field.)
XX SQ Sequence 921 AA;

Query Match      100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRQPAASRDLPFAQBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
DB 1 MRRQPAASRDLPFAQBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQVKEALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKLGCNGLGSPDLPGKPLARLAP 120
DB 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKLGCNGLGSPDLPGKPLARLAP 120
QY 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQRESSV 180
DB 121 DTQVLVPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQRESSV 180
QY 181 APEATQNPPEEAAGQKGGVAYTNQDRKILQCGELYDLDASSLQKVLQYLQQTQASR 240
```

Db 181 APEATQNPEEAAGDQGGVAYTNQDKILQLCGELYDLDASSLQKVLQYQOETQASR 240
QY 241 CCLLLVSEDNLQLSKCVIGDKVLEEBEISFPLTTGRGLGVVDEKKSITQLKDLTSEDMMQQLQ 300
Db 241 CCLLLVSEDNLQLSKCVIGDKVLEEBEISFPLTTGRGLGVVDEKKSITQLKDLTSEDMMQQLQ 300
QY 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360
Db 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360
QY 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLDDQNEL 420
Db 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLDDQNEL 420
QY 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
QY 481 NILCFPIKNEQVIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
Db 481 NILCFPIKNEQVIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAALDSNPFSTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAALDSNPFSTYTPRSLPEDDTSMAIL 600
QY 601 SMLQDMNFNNYKIDCPTLARCLMVKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYN 660
Db 601 SMLQDMNFNNYKIDCPTLARCLMVKGYRPPYHNNMHAFSVSHFCYLLYKNLELTYN 660
QY 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIILNT 720
QY 721 HCCNTPDHSRKYORMLDLMRDIIILATDLAHLRIFKDLQMAEYGVDRTNKQHSLLL 780
Db 721 HCCNTPDHSRKYORMLDLMRDIIILATDLAHLRIFKDLQMAEYGVDRTNKQHSLLL 780
QY 781 CLLMTSCDLSDOTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
Db 781 CLLMTSCDLSDOTGKWKTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELQI 840
QY 841 SPMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFDEEY 900
Db 841 SPMEHIAMPIYKLLQDLPPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFDEEY 900
QY 901 EYVDLDGARAPINGCCSLDAE 921
Db 901 EYVDLDGARAPINGCCSLDAE 921

RESULT 3
AAW18048
ID AAW18048 standard; protein; 921 AA.
XX
AC AAW18048;
XX
DT 25-MAR-2003 (revised)
DT 05-AUG-1997 (first entry)
XX
DE Cyclic-GMP-stimulated phosphodiesterase (cGS-PDE) from p3CGS-5.
XX
KW Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;
KW calcium ion; antibody; cow; polymerase chain reaction.
XX
OS Bos taurus.
XX
PN US5602019-A.
XX
PD 11-FEB-1997.
XX
PF 29-AUG-1994; 94US-00297510.

XX 19-APR-1991; 91US-00688356.
PR 20-APR-1992; 92US-00872644.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
XX
DR WPI; 1997-131799/12.
DR N-PSDB; AAT67220.
XX
PT DNA encoding bovine and human phosphodiesterase enzymes - stimulated by
PT calcium/calmodulin, useful for recombinant prodn. of the enzymes.
XX
PS Example 4; Col 73-78; 69pp; English.
XX
CC The present sequence represents the amino acid sequence from the large
CC open reading frame of p3CGS-5 cDNA bovine adrenal cortex clone insert.
CC The presence of 36 adenosine residues at the 3'-end of the cDNA preceded
CC by a transcription termination consensus sequence suggests that all of
CC the 3' untranslated sequence of the cyclic-GMP-stimulated
CC phosphodiesterase (cGS-PDE) mRNA is represented by this clone. The DNA
CC sequences of the cGS-PDE's are used for the production of the recombinant
CC enzymes, which in turn may be used for antibody production and to screen
CC for compounds that modulate phosphodiesterase activity. (Updated on 25-
CC MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 921 AA;
Query Match 100.0%; Score 4781; DB 2; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRPPAASRDILFAQEPVPRGSGDGLQDALLSLGSLVIVAGLQQAQKALSAPLKVETV 60
Db 1 MRPPAASRDILFAQEPVPRGSGDGLQDALLSLGSLVIVAGLQQAQKALSAPLKVETV 60
QY 61 YTYLLDGSRLVCEBPPELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLAPLAP 120
Db 61 YTYLLDGSRLVCEBPPELPOEGKVRNAVISRKELGNGLGPSDLPGKPLARLAPLAP 120
QY 121 DTQVLVPLVKEAGAAVAVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVPLVKEAGAAVAVILVHCGQLSDNEWSLQAVEKHTLVALKRVQALQORESSV 180
QY 181 APEATQNPEEAAGDQGGVAYTNQDKILQLCGELYDLDASSLQKVLQYQOETQASR 240
Db 181 APEATQNPEEAAGDQGGVAYTNQDKILQLCGELYDLDASSLQKVLQYQOETQASR 240
QY 241 CCLLLVSEDNLQLSKCVIGDKVLEEBEISFPLTTGRGLGVVDEKKSITQLKDLTSEDMMQQLQ 300
Db 241 CCLLLVSEDNLQLSKCVIGDKVLEEBEISFPLTTGRGLGVVDEKKSITQLKDLTSEDMMQQLQ 300
QY 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360
Db 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVLST 360
QY 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLDDQNEL 420
Db 361 LAFQEKQKLKCECOALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFVLDDQNEL 420
QY 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVDESEYIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
QY 481 NILCFPIKNEQVIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
Db 481 NILCFPIKNEQVIGVAELVKNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAALDSNPFSTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAALDSNPFSTYTPRSLPEDDTSMAIL 600

QY 601 SMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPVYHNMHAFSVSHFCYLLYKNLELNTNY 660
 Db 601 SMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPVYHNMHAFSVSHFCYLLYKNLELNTNY 660
 QY 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNT 720
 Db 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNT 720
 QY 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNTKQHLSLL 780
 Db 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNTKQHLSLL 780
 QY 781 CLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 Db 781 CLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
 Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
 QY 901 EVPDLGAPINGCCSLDAE 921
 Db 901 EVPDLGAPINGCCSLDAE 921

RESULT 4

AAW71224
 ID AAW71224 standard; protein; 921 AA.

AC AAW71224;

DT 29-OCT-1998 (first entry)

DE CGS-PDE encoded by p3CGS-5.

KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; Cam-PDE;
 KW assay; identification; modification; enzymatic activity; modulator;
 KW cyclic guanosine monophosphate-stimulated phosphodiesterase; CGS-PDS.

OS Bos sp.

XX US5800987-A.

XX 01-SEP-1998.

XX 31-MAY-1995; 95US-00455525.

XX 19-APR-1991; 91US-00688356.

XX 20-APR-1992; 92US-00872644.

XX 29-AUG-1994; 94US-00297494.

XX (UNIW) UNIV WASHINGTON.

PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;

XX WPI; 1998-494762/42.

DR N-PSDB; AAV54758.

XX Identification of modulators of Calcium/calmodulin sensitive cyclic
 PT nucleotide phosphodiesterase - uses recombinant cells expressing the
 PT enzyme and monitoring protein expression in the presence of potential
 PT modulators.

XX Example 4; Col 73-78; 69pp; English.

XX The present sequence is encoded by a sequence isolated from a bovine
 CC adrenal cortex cDNA library known as cyclic guanosine monophosphate
 CC stimulated phosphodiesterase (CGS-PDE). The specification also describes
 CC Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase (Cam-PDE)
 CC enzymes. Cam-PDE enzymes catalyze the hydrolysis of cyclic nucleotides
 CC and as such control their intracellular level. They are controlled by
 CC second messengers e.g. Ca2+ and calmodulin and transmembrane signals and

CC through pathways involving these, regulate flow of information from
 CC extracellular hormones, neurotransmitters and other signals using cyclic
 CC nucleotides as messengers. The specification describes an assay for
 CC identifying a chemical agent which modifies the enzymatic activity of a
 CC mammalian Cam-PDE. The assays are useful for identifying modulators of
 CC Cam-PDEs. The assay is carried out by incubating cells expressing Cam-PDE
 CC with the suspected modulator and measuring its effect e.g. monitoring the
 CC hydrolysis of cAMP and/or cGMP

XX SQ Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 2; Length 921;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRRQPAASRDLLFAQEPVPPGSGDQALQDALLSLGSDIVAGLQQAQVKEALSAVLPKVETV 60
 Db 1 MRRQPAASRDLLFAQEPVPPGSGDQALQDALLSLGSDIVAGLQQAQVKEALSAVLPKVETV 60
 QY 61 YTYLLDGESRLVCEEPHELPQEGKVRNAVTSRRLGCGNGLGPSPDLGPKPLARLVAPLAP 120
 Db 61 YTYLLDGESRLVCEEPHELPQEGKVRNAVTSRRLGCGNGLGPSPDLGPKPLARLVAPLAP 120
 QY 121 DTQVLVIPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
 Db 121 DTQVLVIPLVDKEAGAAVAAILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
 QY 181 APEATQNPPEAAGDQKGVAVYTNQDKILQCGELYDLDDASSLQKLVQYLOQETQASR 240
 Db 181 APEATQNPPEAAGDQKGVAVYTNQDKILQCGELYDLDDASSLQKLVQYLOQETQASR 240
 QY 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPITTLGRGQVVEDKKSIOIKDLTSDQMQLQ 300
 Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPITTLGRGQVVEDKKSIOIKDLTSDQMQLQ 300
 QY 301 SMLGCEVQAMLCPVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSTVLTST 360
 Db 301 SMLGCEVQAMLCPVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTSTVLTST 360
 QY 361 LAFQEKQKJCECOALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNEL 420
 Db 361 LAFQEKQKJCECOALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNEL 420
 QY 421 VAKVFDGCVVEDESEYIRIPADQGIAGHVATTGQILNPDAVAHPFLVRGVDDSTGFRTR 480
 Db 421 VAKVFDGCVVEDESEYIRIPADQGIAGHVATTGQILNPDAVAHPFLVRGVDDSTGFRTR 480
 QY 481 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNEA 540
 Db 481 NILCFPIKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKNEA 540
 QY 541 QYRSHLANEMMYHMKVSDDEYTKLHDGQOPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
 Db 541 QYRSHLANEMMYHMKVSDDEYTKLHDGQOPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
 QY 601 SMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPVYHNMHAFSVSHFCYLLYKNLELNTNY 660
 Db 601 SMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPVYHNMHAFSVSHFCYLLYKNLELNTNY 660
 QY 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNT 720
 Db 661 LEDMEIFALFTSCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSMERHHPAQAIILNT 720
 QY 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNTKQHLSLL 780
 Db 721 HGCNIFDHFSRKDYQRMOLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNTKQHLSLL 780
 QY 781 CLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 Db 781 CLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
 Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEY 900

Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
 QY 901 EVPDLGAPINGCCSLDAE 921
 Db 901 EVPDLGAPINGCCSLDAE 921
 RESULT 5
 AAW77040
 ID AAW77040 standard; protein; 921 AA.
 AC AAW77040;
 XX
 XX 09-NOV-1998 (first entry)
 DT Adrenal cortex Ca2+/calmodulin stimulated phosphodiesterase.
 DE
 DE Adrenal cortex Ca2+/calmodulin stimulated phosphodiesterase.
 KW ss; cow; Ca2+ stimulated phosphodiesterase;
 KW Calmodulin stimulated phosphodiesterase; therapeutic; antibody.
 XX
 OS Bos sp.
 XX
 XX US5789553-A.
 XX
 XX 04-AUG-1998.
 PD
 XX 31-MAY-1995; 95US-00455526.
 XX
 PR 19-APR-1991; 91US-00688356.
 PR 20-APR-1992; 92US-00872644.
 PR 29-AUG-1994; 94US-00297494.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 XX Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;
 PI
 XX WPI; 1998-446185/38.
 DR N-PSDB; AAV48201.
 XX
 XX Antibody to phosphodiesterase polypeptide - useful for purification or
 PT detection of polypeptide.
 XX
 XX Example 4; Col 65-72; 69pp; English.
 PS
 XX The adrenal cortex Ca2+/calmodulin stimulated phosphodiesterase is one of
 CC several phosphodiesterases isolated in this invention, used to transform
 CC host cells, preferably mammalian or yeast cells. The recombinant proteins
 CC and fragments produced can be used for therapeutic, diagnostic, and
 CC prognostic purposes and will provide the basis for preparation of
 CC monoclonal and polyclonal antibodies. An antibody specific for the
 CC Ca2+/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE)
 CC polypeptide is useful for affinity purification or detection of the
 CC polypeptide and is selective only for the Ca2+/calmodulin stimulated
 CC cyclic nucleotide PDE polypeptide
 XX
 SQ Sequence 921 AA;
 Query Match 100.0%; Score 4781; DB 2; Length 921;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRQPAASRDLPFAQEPVPPGSDGALQDALLSGSVIDVAGLQQAQVKEALSAPLKVETV 60
 Db 1 MRQPAASRDLPFAQEPVPPGSDGALQDALLSGSVIDVAGLQQAQVKEALSAPLKVETV 60
 QY 61 YTYLDGSRSLVCBPPHLPQEGKRVAVISRRKLGCGNGLGPSDLPGKPLARLVAPLAP 120
 Db 61 YTYLDGSRSLVCBPPHLPQEGKRVAVISRRKLGCGNGLGPSDLPGKPLARLVAPLAP 120
 QY 121 DTQNLVILPLVDKEAGAAVILVHCGQSDNEEWSLQAVKHVTLVALKRVQALQRESSV 180
 Db 121 DTQNLVILPLVDKEAGAAVILVHCGQSDNEEWSLQAVKHVTLVALKRVQALQRESSV 180

QY 181 APEATONPPEAAGDQKGGVATVNDQRKILQLCGELYDLDAASSLQALKVLYLQOETQASR 240
 Db 181 APEATONPPEAAGDQKGGVATVNDQRKILQLCGELYDLDAASSLQALKVLYLQOETQASR 240
 QY 241 CCLLLVSEDNLQLSCKVIGDKVLEBESFPLTTGRLGQVVEDKKSILQKDLTSEDWQOLQ 300
 Db 241 CCLLLVSEDNLQLSCKVIGDKVLEBESFPLTTGRLGQVVEDKKSILQKDLTSEDWQOLQ 300
 QY 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLTTST 360
 Db 301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLTTST 360
 QY 361 LAFQKEQKLKCECOALLQVAKNLPFHLDDVSVLLQBIITEARNLSNAECSVPFLLDQNEL 420
 Db 361 LAFQKEQKLKCECOALLQVAKNLPFHLDDVSVLLQBIITEARNLSNAECSVPFLLDQNEL 420
 QY 421 VAKVFDGGVDESSYEIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTR 480
 Db 421 VAKVFDGGVDESSYEIRIPADQGIAGHVATTGQIILNIPDAYAHPLFYRGVDDSTGFRTR 480
 QY 481 NILCFPIKNENQEVIGVAELVNKINGPWFSEKDEDLATAFSIYCGISIAHSLLYKKVNEA 540
 Db 481 NILCFPIKNENQEVIGVAELVNKINGPWFSEKDEDLATAFSIYCGISIAHSLLYKKVNEA 540
 QY 541 QYRSHLANEMMYHMKVSDDEYTKLLHDCIQPVAIDSNFASFYTPRSLPEDDTSMAIL 600
 Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDCIQPVAIDSNFASFYTPRSLPEDDTSMAIL 600
 QY 601 SMLQDMNFNNYKIDCPTLARECLVKKGYRPPVHNMMHAFSVSHFCYLLYKNLELTNY 660
 Db 601 SMLQDMNFNNYKIDCPTLARECLVKKGYRPPVHNMMHAFSVSHFCYLLYKNLELTNY 660
 QY 661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSSEGSVMERHFFAQAIILNT 720
 Db 661 LEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSSEGSVMERHFFAQAIILNT 720
 QY 721 HGCNIFDHFSRKDYORMLDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
 Db 721 HGCNIFDHFSRKDYORMLDLMRDIIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
 QY 781 CULMTSCDLSOOTKGWKTTRKIAELIYKEFFPSQGLEKAWGNRPWEMDMREKAYIPELQI 840
 Db 781 CULMTSCDLSOOTKGWKTTRKIAELIYKEFFPSQGLEKAWGNRPWEMDMREKAYIPELQI 840
 QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
 Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
 QY 901 EVPDLGAPINGCCSLDAE 921
 Db 901 EVPDLGAPINGCCSLDAE 921
 RESULT 6
 AAW60752
 ID AAW60752 standard; protein; 921 AA.
 XX
 AC AAW60752;
 XX
 XX 07-SEP-1998 (first entry)
 DT
 XX CGS-PDE isolated from bovine adrenal cortex.
 DE
 XX Bovine; decrease; intracellular concentration; CAMP; cGMP;
 KW calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterase;
 KW Cam-PDE; therapy; prognosis; diagnosis; specific modulator;
 KW Cam-PDE activity; identification; signalling; extracellular hormone;
 KW neurotransmitter; selective inhibitor; cardiotoxic; antidepressant;
 KW antihypertensive; antithrombotic agent;
 KW cyclic-GMP-nucleotide phosphodiesterase; CDS-PDE.
 XX
 XX Bos sp.
 XX

PN US5776752-A.
 XX
 PD 07-JUL-1998.
 XX
 XX 07-JUN-1995; 95US-00479532.
 PF
 XX 19-APR-1991; 91US-00688356.
 PR 20-APR-1992; 92US-00872644.
 PR 29-AUG-1994; 94US-00297494.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
 XX WPI, 1998-398038/34.
 XX N-PSDB; AAV36153.
 DR
 XX New calmodulin and calcium stimulated cyclic nucleotide phosphodiesterase
 PT - used e.g to identify selective modulators, potentially useful as e.g.
 PT cardiotonic, antidepressant, antihypertensive agents.
 XX
 PS Example 4; Col 71-76; 69pp; English.
 XX
 CC The present sequence represents a cyclic-GMP-nucleotide phosphodiesterase
 CC (cgs-PDE) polypeptide isolated from bovine adrenal cortex. The
 CC specification describes calcium ion/calmodulin stimulated cyclic
 CC nucleotide phosphodiesterases (Cam-PDEs). Cam-PDEs are characterised by
 CC their responsiveness to intracellular calcium, which leads to a decreased
 CC intracellular concentration of cAMP and/or cGMP. Cam-PDEs, and their
 CC fragments or synthetic peptides, are used in therapy, prognosis and
 CC diagnosis. They are also used to generate specific antibodies useful as
 CC immunoassay reagents for detecting the protein or for affinity
 CC purification and for identifying specific modulators of Cam-PDE activity.
 CC Cam-PDEs are implicated in signalling involving extracellular hormones
 CC and neurotransmitters, so selective inhibitors are potentially useful as
 CC cardiotonic, antidepressant, antihypertensive and antithrombotic agents
 XX
 SQ Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 2; Length 921;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRQPAASRDLPAGEPVPVPGSGDGLQDALLSLGSDVVDVAGLQAVKEALSAPLKVETV 60
 Db |||||
 Qy 1 MRQPAASRDLPAGEPVPVPGSGDGLQDALLSLGSDVVDVAGLQAVKEALSAPLKVETV 60
 Db |||||
 Qy 61 YTYLLDGSRLVCEPPELHPEQGVREAVISRKELGCGNGLGSDLPCKPLARLVAPLAP 120
 Db |||||
 Qy 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
 Db |||||
 Qy 121 DTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
 Db |||||
 Qy 181 APEATONPEEAAGDQGVATYNDQKILQCGELYDLDDASSLQKVLQVLOQETQASR 240
 Db |||||
 Qy 181 APEATONPEEAAGDQGVATYNDQKILQCGELYDLDDASSLQKVLQVLOQETQASR 240
 Db |||||
 Qy 241 CCLLVSDNQLQSKVIGDKVLEBEEISFPITTTGRLGQVVDKKSQIKDLTSDMQQLQ 300
 Db |||||
 Qy 241 CCLLVSDNQLQSKVIGDKVLEBEEISFPITTTGRLGQVVDKKSQIKDLTSDMQQLQ 300
 Db |||||
 Qy 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVHCFHYTSTVLST 360
 Db |||||
 Qy 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVHCFHYTSTVLST 360
 Db |||||
 Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAICSVFLLDQNEL 420
 Db |||||
 Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAICSVFLLDQNEL 420
 Db |||||
 Qy 421 VAKVFDGCVGVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
 Db |||||

Db 421 VAKVFDGCVGVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
 Qy 481 NILCFPIKNENQEVIGVAELVKNKINGPWFSEFDEDLATAPSIYCGISIAHSLLYKKVNEA 540
 Db |||||
 Db 481 NILCFPIKNENQEVIGVAELVKNKINGPWFSEFDEDLATAPSIYCGISIAHSLLYKKVNEA 540
 Qy 541 QYRSHLANEMMMYHMKVSDDEYTKLLHDGIDQVAAIDSNFASFTVTPRSLPEDDTSMAIL 600
 Db |||||
 Db 541 QYRSHLANEMMMYHMKVSDDEYTKLLHDGIDQVAAIDSNFASFTVTPRSLPEDDTSMAIL 600
 Qy 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPVPHNMHAFSVSHFCYLLYKNLELTYN 660
 Db |||||
 Db 601 SMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPVPHNMHAFSVSHFCYLLYKNLELTYN 660
 Qy 661 LEDMEIFALFISCHDLDRGTNNSQVASKSVLAALYSSEGSVMERHHAQAIAIANT 720
 Db |||||
 Db 661 LEDMEIFALFISCHDLDRGTNNSQVASKSVLAALYSSEGSVMERHHAQAIAIANT 720
 Qy 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
 Db |||||
 Db 721 HGCNIFDHFSRKDYQRMLDLMDRIILATDLAHLRIFKDLQMAEVGYDRTNKQHSLLL 780
 Qy 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 Db |||||
 Db 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEPFSQGDLEKAMGNRPMEMMDREKAYIPELQI 840
 Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVANSREHWTKVSHKFTIRGLPSNNSLDPLDEEY 900
 Db |||||
 Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVANSREHWTKVSHKFTIRGLPSNNSLDPLDEEY 900
 Qy 901 EVPLDGDARAPINGCCSLDAE 921
 Db |||||
 Db 901 EVPLDGDARAPINGCCSLDAE 921

RESULT 7
 AAY80984
 ID AAY80984 standard; protein; 921 AA.
 AC AAY80984;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE Bovine adrenal cortex cgs-PDE, SEQ ID NO:39.
 XX
 KW Phosphodiesterase; calcium; calmodulin; cyclic guanine monophosphate;
 KW cGMP; cyclic nucleotide; messenger; signal transduction; regulation;
 KW inhibitor; cardiotonic; antidepressant; antihypertensive; antithrombotic.
 XX
 OS Bos taurus.
 XX
 FN US6015677-A.
 XX
 PD 18-JAN-2000.
 XX
 PF 25-AUG-1998; 98US-00139491.
 XX
 PR 19-APR-1991; 91US-00688356.
 PR 20-APR-1992; 92US-00872644.
 PR 29-AUG-1994; 94US-00297494.
 PR 31-MAY-1995; 95US-00455525.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 XX Charbonneau H, Sonnenburg WK, Bentley KJ, Beavo JA;
 FI WPI, 2000-181142/16.
 DR N-PSDB; AAZ90377.
 XX
 XX Assay for inhibitors of cyclic guanine monophosphate-stimulated
 PT nucleotide phosphodiesterase, potentially useful as cardiotonic agents,
 PT from their ability to alter a heat-shock phenotype.
 XX

PS	Claim 1; Col 71-76; 69pp; English.	
XX	The invention relates to purified and isolated nucleotide sequences encoding mammalian Ca ²⁺ /calmodulin-stimulated phosphodiesterases (Cam-PDEs) and cyclic guanine monophosphate (cGMP)-stimulated phosphodiesterases (cGS-PDEs). In particular the invention relates to an assay for identifying chemicals that modify the enzymatic activity of a mammalian cGS-PDE. The PDEs catalyze the hydrolysis of cyclic nucleotides to their corresponding 5'-nucleoside monophosphates. In this way they control the cellular concentration of cyclic nucleotides, thereby regulating the flow of information from extracellular hormones, neurotransmitters or other signals that use cyclic nucleotides as messengers. The PDEs in turn are regulated by transmembrane signals or second messenger ligands such as Ca ²⁺ or cGMP. Inhibitors of these enzymes are potentially useful as cardiotonics, antidepressants, antihypertensives or antithrombotics. The method of the invention can identify specific inhibitors of particular isoforms of cGS-PDEs. Sequences AAY80968, AAY80972, AAY80975, AAY80977, AAY80984-Y80986, and AAY80988-Y80990 represent isoforms of Cam-PDEs and cGS-PDEs from bovines and humans	
XX	Sequence 921 AA;	
SQ	Query Match Best Local Similarity 100.0%; Score 4781; DB 3; Length 921; Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MRQPAASRDLEPAQEPVPGSGDQALQDALLSLGSLVQVAGLQQAQVKEALSAPLKVETV 60	661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALNT 720
DB	1 MRQPAASRDLEPAQEPVPGSGDQALQDALLSLGSLVQVAGLQQAQVKEALSAPLKVETV 60	721 HGCNIFDHFESRKYQRMQLDMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKQHSLLL 780
QY	61 YTYLLDGESRLVCEBPPELPOEGKVREAVISRKRLGCGNLGSPDLPGKPLARLAPLAP 120	721 HGCNIFDHFESRKYQRMQLDMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKQHSLLL 780
DB	61 YTYLLDGESRLVCEBPPELPOEGKVREAVISRKRLGCGNLGSPDLPGKPLARLAPLAP 120	781 CLIMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
QY	121 DTQVLVIPLVDKEAGNAVILVHCGQLSDNEWSLQAVEKHTLVALKRQVQLQRESSV 180	781 CLIMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
DB	121 DTQVLVIPLVDKEAGNAVILVHCGQLSDNEWSLQAVEKHTLVALKRQVQLQRESSV 180	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHMTKVSHKPTIRGLPSNNSLDFLDEEY 900
QY	181 APEATQNPPEAAGDKGVATVNDQRKILQCGELYDLDASSLQKLVQYLOQETQASR 240	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHMTKVSHKPTIRGLPSNNSLDFLDEEY 900
DB	181 APEATQNPPEAAGDKGVATVNDQRKILQCGELYDLDASSLQKLVQYLOQETQASR 240	901 EYVPLDGGARAPINGCCSLDAE 921
QY	241 CCLLVSEDNLQSKVIGDKVLEEBISFPLTTGRIGQVVEDKSIQLKDLTSEDQQQLQ 300	901 EYVPLDGGARAPINGCCSLDAE 921
DB	241 CCLLVSEDNLQSKVIGDKVLEEBISFPLTTGRIGQVVEDKSIQLKDLTSEDQQQLQ 300	901 EYVPLDGGARAPINGCCSLDAE 921
QY	301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTST 360	901 EYVPLDGGARAPINGCCSLDAE 921
DB	301 SMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTST 360	901 EYVPLDGGARAPINGCCSLDAE 921
QY	361 LAFQKEQKLCRCQALLQVAKNLFTHLDDVSVLLQBIITEARNLSNABICSVPLDDQNEL 420	901 EYVPLDGGARAPINGCCSLDAE 921
DB	361 LAFQKEQKLCRCQALLQVAKNLFTHLDDVSVLLQBIITEARNLSNABICSVPLDDQNEL 420	901 EYVPLDGGARAPINGCCSLDAE 921
QY	421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRT 480	901 EYVPLDGGARAPINGCCSLDAE 921
DB	421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYHPLFYRGVDDSTGFRT 480	901 EYVPLDGGARAPINGCCSLDAE 921
QY	481 NILCPPIKNEQEVIGVABLNVKINGPWFPSKFEDEDLATAFSIYCGISIAHSLLYKKVNEA 540	901 EYVPLDGGARAPINGCCSLDAE 921
DB	481 NILCPPIKNEQEVIGVABLNVKINGPWFPSKFEDEDLATAFSIYCGISIAHSLLYKKVNEA 540	901 EYVPLDGGARAPINGCCSLDAE 921
QY	541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQVPAIDNSFASFTYTPRSLPDDTSMALL 600	901 EYVPLDGGARAPINGCCSLDAE 921
DB	541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIQVPAIDNSFASFTYTPRSLPDDTSMALL 600	901 EYVPLDGGARAPINGCCSLDAE 921
QY	601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRPPYHNMWHAFSVSHFCVLLYKNLELNTY 660	901 EYVPLDGGARAPINGCCSLDAE 921
DB	601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRPPYHNMWHAFSVSHFCVLLYKNLELNTY 660	901 EYVPLDGGARAPINGCCSLDAE 921
QY	661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALNT 720	901 EYVPLDGGARAPINGCCSLDAE 921

Db	661 LEDMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALNT 720
QY	721 HGCNIFDHFESRKYQRMQLDMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKQHSLLL 780
Db	721 HGCNIFDHFESRKYQRMQLDMRDIIILATDLAHLRIFFKDLQKMAEYGYDRTNKQHSLLL 780
QY	781 CLIMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
Db	781 CLIMTSCDLSQDTKGWKTTRKIAELIYKFFSQGDLEKAMGNRPMEMDREKAYIPELQI 840
QY	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHMTKVSHKPTIRGLPSNNSLDFLDEEY 900
Db	841 SPMEHIAPIYKLLQDLPPKAAELVERVASNREHMTKVSHKPTIRGLPSNNSLDFLDEEY 900
QY	901 EYVPLDGGARAPINGCCSLDAE 921
Db	901 EYVPLDGGARAPINGCCSLDAE 921
RESULT 8	
ABU58723	
ID	ABU58723 standard; protein; 921 AA.
XX	
AC	ABU58723;
XX	
DT	15-APR-2003 (first entry)
XX	
DE	Bovine adrenal cortex cGS-PDE.
XX	
KW	Cow; Ca ²⁺ /calmodulin stimulated phosphodiesterase; enzyme; Cam-PDE;
KW	59Kda Cam-PDE; 61kda Cam-PDE; 63kda Cam-PDE; cGS-PDE;
KW	cyclic-GMP-stimulated phosphodiesterase; cardiotoxic agent;
KW	antidepressant; anti-hypertensive; anti-thrombotic.
OS	Bos taurus.
XX	
PN	US2002151024-A1.
XX	
PD	17-OCT-2002.
XX	
PF	18-JUN-2001; 2001US-00883825.
XX	
PR	19-APR-1991; 91US-00688356.
PR	20-APR-1992; 92US-00872644.
PR	31-MAY-1995; 95US-00455526.
PR	28-JUL-1998; 98US-00123783.
XX	
PA	(UNITW) UNIV WASHINGTON.
XX	
PI	Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
XX	
DR	WPI; 2003-198291/19.
XX	
DR	N-PSDB; ABX78854.
XX	
PT	New purified and isolated DNA sequence encoding a mammalian
PT	calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide
PT	phosphodiesterase polypeptide, useful for therapeutic, diagnostic and
XX	prognostic applications.
PS	Example 4; Page 39-42; 71pp; English.
XX	
CC	The invention relates to purified and isolated polynucleotide sequence
CC	encoding a mammalian Ca ²⁺ /calmodulin- or cyclic GMP-stimulated cyclic
CC	nucleotide phosphodiesterase polypeptide (Cam-PDE and cGS-PDE). Also
CC	included are a DNA vector comprising the novel DNA sequence, a host cell
CC	transformed with the polynucleotide sequence, a polypeptide product of
CC	the expression in the transformed host cell, an antibody specifically
CC	immunoreactive with the polypeptide and assay methods for identifying a
CC	chemical agent which modifies the enzymatic activity of a mammalian CamP-
CC	PDE or cGS-PDE. Disclosed are the cDNA and protein sequences of bovine
CC	59Kda Cam-PDE, 61kda Cam-PDE, 63kda Cam-PDE, cGS-PDE and human 61kda Cam-
CC	PDE and cGS-PDE. The DNA sequence is useful for producing a polypeptide
CC	having the enzymatic activity of a mammalian Cam-PDE or cGS-PDE which is

CC used in therapeutic, diagnostic and prognostic applications and in the
CC preparation of antibodies. Isolated chemical agents which are inhibitors
CC of PDEs may have anti-depressant, anti- hypertensive or anti-thrombotic
CC activities or may be cardiotoxic agents. The present sequence is a Bovine
XX CaM-PDE or CGS-PDE (or fragment) of the invention
SQ Sequence 921 AA;

Query Match 100.0%; Score 4781; DB 6; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRROPASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQKALSAVLPKVETV 60
Db 1 MRROPASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQKALSAVLPKVETV 60
Qy 61 YTYLLDGSRLVCEPPEPHELPOGKVRBAVTSRKELGKGLGSPDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEPPEPHELPOGKVRBAVTSRKELGKGLGSPDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVIFLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVIFLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Qy 181 APEATQNPPEAAGDQKGVATYNDKRIQLCGELYDLDASSLQQLVLYLQOSTQASR 240
Db 181 APEATQNPPEAAGDQKGVATYNDKRIQLCGELYDLDASSLQQLVLYLQOSTQASR 240
Qy 241 CCLLVSDNLIQLSKVIGDKVLEBESIFPLTTGRLGQVVEDKKSQIKLDTSDMQQLQ 300
Db 241 CCLLVSDNLIQLSKVIGDKVLEBESIFPLTTGRLGQVVEDKKSQIKLDTSDMQQLQ 300
Qy 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTST 360
Db 301 SMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTST 360
Qy 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy 421 VAKVFDGCVGVEDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRT 480
Db 421 VAKVFDGCVGVEDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRT 480
Qy 481 NILCFPIKNEQVIGVAVLNKNGPWFSPFDEDLATAFSIYCGISTAHSLLYKKNEA 540
Db 481 NILCFPIKNEQVIGVAVLNKNGPWFSPFDEDLATAFSIYCGISTAHSLLYKKNEA 540
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGPVAIDSNFASFTVTPRSLPDDTSMALL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHDGIGPVAIDSNFASFTVTPRSLPDDTSMALL 600
Qy 601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRDPDPYHNMWHAFSVSHFCYLLYKNLELTNY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKGYRDPDPYHNMWHAFSVSHFCYLLYKNLELTNY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGVSMEHHFAQAIILNT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGVSMEHHFAQAIILNT 720
Qy 721 HGCNIFDHFSRKDYRMLDLARDIILATDLAHLRI FKDLQMAEVGYDRTNKQHSLLL 780
Db 721 HGCNIFDHFSRKDYRMLDLARDIILATDLAHLRI FKDLQMAEVGYDRTNKQHSLLL 780
Qy 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRMWMDREKAYIPELQI 840
Db 781 CLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRMWMDREKAYIPELQI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDEY 900
Qy 901 EVPDLDGARAPINGCCSLDAE 921

Db 901 EVPDLDGARAPINGCCSLDAE 921
RESULT 9
ADQ94959
ID ADQ94959 standard; protein; 921 AA.
XX
AC ADQ94959;
XX
DT 23-SEP-2004 (first entry)
XX
Bovine p3CGS-5 clone insert cDNA encoding protein.
XX
CaM-PDE;
KW Ca 2+/ calmodulin stimulated cyclic nucleotide phosphodiesterase; cGMP;
KW cyclic-guanosine monophosphate; cGS-PDE;
KW cyclic-GMP stimulated cyclic nucleotide phosphodiesterase; bovine.
XX
OS Bos sp.
XX
FN US2004126866-A1.
XX
PD 01-JUL-2004.
XX
PF 30-OCT-2003; 2003US-00697894.
XX
PR 19-APR-1991; 91US-00688356.
PR 20-APR-1992; 92US-00872644.
PR 29-AUG-1994; 94US-00297494.
PR 31-MAY-1995; 95US-00455526.
PR 28-JUL-1998; 98US-00123783.
PR 18-JUN-2001; 2001US-00883825.
XX
PA (BEAV/) BEAVO J A.
PA (BENT/) BENTLEY J K.
PA (CHAR/) CHARBONNEAU H.
PA (SONN/) SONNENBURG W K.
FI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
XX
DR WPI; 2004-516912/49.
DR N-PSDB; ADQ94958.
XX
PT Novel mammalian calcium/calmodulin stimulated cyclic phosphodiesterase
PT nucleotide sequence useful for identifying chemical agent that modifies
PT enzymatic activity of calcium/calmodulin stimulated cyclic
PT phosphodiesterase polypeptide.
XX
Example 4; SEQ ID NO 39; 72pp; English.
XX
The present invention provides a mammalian Ca 2+/ calmodulin stimulated
CC cyclic nucleotide phosphodiesterase (CaM-PDE) and cyclic-guanosine
CC monophosphate (cGMP) stimulated cyclic nucleotide phosphodiesterase (CGS-
CC PDE) polypeptide and its polynucleotide. The invention is useful for
CC producing a polypeptide having enzymatic activity of mammalian CaM-PDE
CC and CGS-PDE. The invention is also useful for identifying a chemical
CC agent that modifies the enzymatic activity of mammalian CaM-PDE and CGS-
CC PDE. The present sequence is bovine p3CGS-5 clone insert cDNA encoding
CC protein.
SQ Sequence 921 AA;
Query Match 100.0%; Score 4781; DB 8; Length 921;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 921; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRROPASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQKALSAVLPKVETV 60
Db 1 MRROPASRDLPFAQEPVPPGSGDGLQDALLSLGSLVDVAGLQQAQKALSAVLPKVETV 60
Qy 61 YTYLLDGSRLVCEPPEPHELPOGKVRBAVTSRKELGKGLGSPDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEPPEPHELPOGKVRBAVTSRKELGKGLGSPDLPGKPLARLVAPLAP 120
Qy 901 EVPDLDGARAPINGCCSLDAE 921

Db 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKRLGCGNGLSPDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVKHTLVALKRVQALQOQRESSV 180
Db 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVKHTLVALKRVQALQOQRESSV 180
Qy 181 APEATONPPEEAAGDQKGGVATVNDQRKTLQCGELYDLASSLQIKVLYQLOQTOASR 240
Db 181 APEATONPPEEAAGDQKGGVATVNDQRKTLQCGELYDLASSLQIKVLYQLOQTOASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMQOLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMQOLQ 300
Qy 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360
Db 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360
Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRT 480
Db 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRT 480
Qy 481 NILCFPIKNENQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNV 540
Db 481 NILCFPIKNENQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNV 540
Qy 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEYTKLLHGGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Qy 601 SMLQDMFNINNYKIDCPTLAFCLMVKGYRDPVYHNMHAFSVSHFCVLLYKNLELNY 660
Db 601 SMLQDMFNINNYKIDCPTLAFCLMVKGYRDPVYHNMHAFSVSHFCVLLYKNLELNY 660
Qy 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSMVRRHFAQAIALNT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALYSSEGSMVRRHFAQAIALNT 720
Qy 721 HGCNIFDHFSDKDYQMLDLARDIILATDLAHLRIFKDLQMAEVGYDRTNKHHSLLL 780
Db 721 HGCNIFDHFSDKDYQMLDLARDIILATDLAHLRIFKDLQMAEVGYDRTNKHHSLLL 780
Qy 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELOI 840
Db 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLKAMGNRPMEMMDREKAYIPELOI 840
Qy 841 SFMEHIAMPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVAENREHWTKVSHKFTIRGLPSNNSLDFLDEY 900
Qy 901 EVPDLGAPINGCCSLDAE 921
Db 901 EVPDLGAPINGCCSLDAE 921

RESULT 10

AAR28407
ID AAR28407 standard; protein; 921 AA.

XX AC AAR28407;

XX DT 25-MAR-2003 (revised)

XX DT 19-MAR-1993 (first entry)

XX DT cGS-PDE from clone 3CGS-5, from bovine adrenal cortex.

XX DE Cyclic GMP; stimulated; cyclic; nucleotide; phosphodiesterase.

XX KW Bos taurus.

XX OS

XX FN WO9218541-A1.
XX PD 29-OCT-1992.
XX PF 20-APR-1992; 92WO-US003222.
XX PR 19-APR-1991; 91US-00688356.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK,
XX DR WPI; 1992-382051/46.
XX DR N-PSDB; AAQ30180.
XX PT New DNA encoding mammalian cyclic nucleotide phospho-di-esterase - and
XX PT derived vectors and host cells, useful for screening cpds. for inhibitory
XX PT or activating activity.
XX PS Example 4; Page 83; 133pp; English.
XX CC An unamplified bovine adrenal cortex cDNA library was prepd. and screened
XX CC with redundant 23-mer antisense oligonucleotide probes end labelled with
XX CC radiolabelled ATP and T4 polynucleotide kinase. A single 2.1 kb cDNA
XX CC clone (designated pCGS-3.2.1) was obt'd. This clone was used to screen a
XX CC second, amplified bovine adrenal cortex cDNA library to yield 52 putative
XX CC clones. The largest insert was of 4.2 kb in a plasmid designated p3CGS-5.
XX CC The cDNA encodes a 921 residue protein with mol. wt. 103 kD. (Updated on
XX CC 25-MAR-2003 to correct PN field.)
XX SQ Sequence 921 AA;

Query Match 99.6%; Score 4764; DB 2; Length 921;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 918; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MRRQPAASRDILFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVT 60
Db 1 MRRQPAASRDILFAQEPVPPGSGDQALQDALLSLGSDVIDVAGLQQAQVKEALSAVLPKVT 60
Qy 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKRLGCGNGLSPDLPGKPLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEBPPELPOEGKREAVISRKRLGCGNGLSPDLPGKPLARLVAPLAP 120
Qy 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVKHTLVALKRVQALQOQRESSV 180
Db 121 DTQVLVPLVDKEAGAAVAVILVHCCQLSDNEWSLQAVKHTLVALKRVQALQOQRESSV 180
Qy 181 APEATONPPEEAAGDQKGGVATVNDQRKTLQCGELYDLASSLQIKVLYQLOQTOASR 240
Db 181 APEATONPPEEAAGDQKGGVATVNDQRKTLQCGELYDLASSLQIKVLYQLOQTOASR 240
Qy 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMQOLQ 300
Db 241 CCLLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLGVVDEKSIQKDLTSEDMQOLQ 300
Qy 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360
Db 301 SMLGCEVQAMLCVVISRATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLST 360
Qy 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
Qy 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRT 480
Db 421 VAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFVRGVDDSTGFRT 480
Qy 481 NILCFPIKNENQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNV 540
Db 481 NILCFPIKNENQEVIGVAELVKNKINGPWFKFDLATAFSIYCGISIAHSLLYKKNV 540

QY 541 QYRSHLANEMMMYHKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
DB 541 QYRSHLANEMMMYHKVSDDEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
QY 601 SMLQDMNFNNYKIDCPTLARFCFLMVKKGYRDPDPYHNMWHAHSVSHFCYLLYKNLELTNY 660
DB 601 SMLQDMNFNNYKIDCPTLARFCFLMVKKGYRDPDPYHNMWHAHSVSHFCYLLYKNLELTNY 660
QY 661 LEDMEIFALFTSCWCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNT 720
DB 661 LEDMEIFALFTSSWCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNT 720
QY 721 HGCNIFDHFSPKDYORMLDLMRDIIILATDLAHLRIIFKDLQKMAEVGYDRTNKHHSLLL 780
DB 721 HGCNIFDHFSPKDYORMLDLMRDIIILATDLAHLRIIFKDLQKMAEVGYDRTNKHHSLLL 780
QY 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFTSQGDLEKAMGNRPMEWMDREKAYIPELQI 840
DB 781 CLMTSCDLSQDTKGWKTTRKIAELIYKEFTSQGDLEKAMGNRPMEWMDREKAYIPELQI 840
QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
DB 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEY 900
QY 901 EVDPLDGARAPINGCCSLDAE 921
DB 901 EVDPLDGARAPINGCCSLDAE 921

RESULT 11

AA869728
ID AA869728 standard; protein; 942 AA.

XX AC AA869728;

XX DT 25-MAR-2003 (revised)

XX DT 11-OCT-1995 (first entry)

XX CYCLIC-GMP stimulated nucleotide PDE clone pBBCGSPDE-7.

XX CYCLIC-GMP stimulated nucleotide phosphodiesterase; antibodies;

XX KW bovine adrenal cortex; hormones; neurotransmitters;

XX KW transmission regulation; enzyme purification; clone pBBCGSPDE-7.

XX OS Bos taurus.

XX PN US5389527-A.

XX PD 14-FEB-1995.

XX PF 20-APR-1992; 92US-00872644.

XX PR 19-APR-1991; 91US-00688356.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Sonnenburg WK, Charbonneau H, Beavo JA;

XX DR WPI; 1995-090205/12.

XX DR N-PSDB; AAQ83977.

XX PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phosphodiesterase - and related vectors and transformed cells, useful for screening cpds. for phospho-di:esterase modulating activity.

XX PS Example 5; Col 79-86; 69pp; English.

XX CC AAQ83977 encodes AA869728 the bovine brain cyclic-GMP stimulated

XX CC nucleotide phosphodiesterase (Cam PDE) clone pBBCGSPDE-7. Eukaryotic

XX CC cells that express Cam PDE can be used to screen cpds. for the ability to

XX CC modulate Cam PDE activity. Cam PDEs are involved in regulating the

XX CC transmission of information from hormones, neurotransmitters or other

XX CC systems that use cyclic nucleotides as messengers. Antibodies raised

CC against Cam PDE can be used for enzyme purificn., or determination.
CC (Updated on 25-MAR-2003 to correct Pf field.)

XX SQ Sequence 942 AA;

Query Match 97.4%; Score 4657; DB 2; Length 942;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 14 QEPVPPSGDGLQDALLSGSIDVAGLQAAVKESAVLPKVTETVYTYLLDGSRLVC 73

DB 35 EPPPPQPCADSLQDALLSGSIDVAGLQAAVKESAVLPKVTETVYTYLLDGSRLVC 94

QY 74 EEPHPELPQEGKVEAVISRKLGCCNGIGPSDLPGLARLVARLADPTQVLVPLVDKE 133

DB 95 EEPHPELPQEGKVEAVISRKLGCCNGIGPSDLPGLARLVARLADPTQVLVPLVDKE 154

QY 134 AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEAA 193

DB 155 AGAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEAA 214

QY 194 GDQGGVAYTNQDRKILQCGELYDLDASSLQKLVQLVQOETQASRCCLLLVSEDNLQL 253

DB 215 GDQGGVAYTDQDRKILQCGELYDLDASSLQKLVQLVQOETQASRCCLLLVSEDNLQL 274

QY 254 SKVIGDKVLEEEISFPILTTRGLGQVVEDKKS IQLKDLTSEDMOQLQSMGLGCEVQAMLCV 313

DB 275 SKVIGDKVLEEEISFPILTTRGLGQVVEDKKS IQLKDLTSEDMOQLQSMGLGCEVQAMLCV 334

QY 314 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTTSTLAFQEKQKCEC 373

DB 335 PVISRATDQVVALACAFNKLGGDLFTDQDEHVIQCFHYTSTVLTTSTLAFQEKQKCEC 394

QY 374 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGGVVEDE 433

DB 395 QALLQVAKNLFTHLDVSVLLQEIITEARNLSNAEICSVFLLDQNELVAKVDFDGGVVEDE 454

QY 434 SYEIRIPADOGIAGHVATTGOILNIPDAYAPLPYRGVDDSTGPRTRNLCFPKNEQ 493

DB 455 SYEIRIPADOGIAGHVATTGOILNIPDAYAPLPYRGVDDSTGPRTRNLCFPKNEQ 514

QY 494 VIGVAELVNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553

DB 515 VIGVAELVNKINGPWFSPKFDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574

QY 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 613

DB 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMLQDMNFNNYK 634

QY 614 IDCPTLARFCFLMVKKGYRDPDPYHNMWHAHSVSHFCYLLYKNLELTNYLEDMEIFALFTSC 673

DB 635 IDCPTLARFCFLMVKKGYRDPDPYHNMWHAHSVSHFCYLLYKNLELTNYLEDMEIFALFTSC 694

QY 674 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHSRKD 733

DB 695 MCHDLDRGTNNNSFOVASKSVLAALYSSEGSMERHHPAQAIILNTHGNCNIFDHSRKD 754

QY 734 YQRLDLMRDIILATDLAHLRIIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQDT 793

DB 755 YQRLDLMRDIILATDLAHLRIIFKDLQKMAEVGYDRTNKHHSLLCLLMTSCDLSQDT 814

QY 794 KGWKTTRKIAELIYKEFTSQGDLEKAMGNRPMEWMDREKAYIPELQISFMHIAMPIYKL 853

DB 815 KGWKTTRKIAELIYKEFTSQGDLEKAMGNRPMEWMDREKAYIPELQISFMHIAMPIYKL 874

QY 854 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYVPLDGDARAPIN 913

DB 875 LQDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDFLDEEYVPLDGDARAPIN 934

QY 914 GCCSLDAE 921

DB 935 GCCSLDAE 942

Db 95 EEPHELPEGKVRREAVISRKRLGNCGLGPSDLPGKPLARLVAPLAPDTQVIVIPLVNKE 154
Qy 134 AGAVAAVILVHCGQLSDNEEWSLQAVEGHITLVALKRVQALQORESSVAPEATONPPBEAA 193
Db 155 AGAVAAVILVHCGQLSDNEEWSLQAVEGHITLVALKRVQALQORESSVAPEATONPPBEAA 214
Qy 194 GDQGGVAYTQDRKILQLCGELYDLDAASSLQKVLQVLYLQOQTOASRCCLLLVSEDNLQL 253
Db 215 GDQGGVAYTQDRKILQLCGELYDLDAASSLQKVLQVLYLQOQTOASRCCLLLVSEDNLQL 274
Qy 254 SKCVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKOLITSEDMQOLQSMLGCEVQAMLCV 313
Db 275 SKCVIGDKVLEEEISFPITTRGLQGVVEDKKSIIQLKOLITSEDMQOLQSMLGCEVQAMLCV 334
Qy 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFFHTSTVLTSTLAFQKEOKLKCEC 373
Db 335 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFFHTSTVLTSTLAFQKEOKLKCEC 394
Qy 374 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE 433
Db 395 QALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE 454
Qy 434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQE 493
Db 455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNLCFPIKNENQE 514
Qy 494 VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 515 VIGVAELVNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 574
Qy 554 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 613
Db 575 HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYK 634
Qy 614 IDCPTLARFCLMVKKGYRDPYPHNWMAFSVSHFCYLLYKNLENTNYLEDMEIFALFISC 673
Db 635 IDCPTLARFCLMVKKGYRDPYPHNWMAFSVSHFCYLLYKNLENTNYLEDMEIFALFISC 694
Qy 674 MCHDLDRHGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIAILNTHGCMIFDHFSRKD 733
Db 695 MCHDLDRHGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIAILNTHGCMIFDHFSRKD 754
Qy 734 YQRMLDLMDRIILATDLAHLRIFKLOKMAEVGYDRTNKQHSILLCCLMTSCDLSDOT 793
Db 755 YQRMLDLMDRIILATDLAHLRIFKLOKMAEVGYDRTNKQHSILLCCLMTSCDLSDOT 814
Qy 794 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL 853
Db 815 KGWKTTRKIAELIYKEFFSQGDLEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKL 874
Qy 854 LQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDBEYEVDPDLGARAPIN 913
Db 875 LQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLPSNNSLDFLDBEYEVDPDLGARAPIN 934
Qy 914 GCCSLDAE 921
Db 935 GCCSLDAE 942

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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:56 ; Search time 128.535 Seconds
(without alignments)
3669.244 Million cell updates/sec

Title: US-10-697-894-39
Perfect score: 4781
Sequence: 1 MRQPASRDLPAGPVPFG.....VPDLGARAPINGCCSLDAE 921

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4781	100.0	921	1	PI4099 bos taurus
2	4474.5	93.6	941	1	000408 homo sapien
3	4466.5	93.4	941	2	081W54
4	4426	92.6	916	1	Q922s4 mus musculus
5	4324.5	90.5	928	1	Q01062 rattus norv
6	3229	67.5	685	2	Q62MR1
7	1661	34.7	819	2	Q96076
8	1236	25.9	491	2	Q7Q4A0
9	992	20.7	1544	2	Q8MCW0
10	991	20.7	934	2	Q9HCR9
11	991	20.7	988	2	Q96S76
12	991	20.7	1018	2	Q95TW8
13	991	20.7	1131	2	Q9VF19
14	983	20.6	1365	2	Q9VJ79
15	979	20.5	935	2	Q8VID6
16	945	19.8	1088	2	Q7QB99
17	938	19.6	856	2	Q65ZC7
18	938	19.6	859	1	YN56_CABEL
19	924	19.3	883	2	Q6S9E8
20	920.5	19.3	684	2	Q9CZY7
21	917.5	19.2	852	2	Q6S9E9
22	916.5	19.2	779	2	Q6FXH1
23	916	19.2	789	2	Q9ULW9
24	915	19.1	794	2	Q9QYJ6
25	914.5	19.1	779	1	CN10_HUMAN
26	913.5	19.1	788	2	Q9QYJ5
27	909	19.0	796	2	Q6C21
28	908	19.0	843	2	Q7ZW87
29	907.5	19.0	773	2	Q7TFG1
30	907.5	19.0	779	2	Q9WV11
31	907.5	19.0	790	2	Q8CA95

32	907.5	19.0	797	2	Q7TPG2	Q7TPG2 mus musculus
33	906.5	19.0	685	2	Q8VID7	Q8VID7 rattus norv
34	902	18.9	714	2	Q6S9E7	Q6S9E7 rattus norv
35	901	18.8	653	2	Q6S9E6	Q6S9E6 rattus norv
36	900	18.8	714	2	Q9HCP9	Q9HCP9 homo sapien
37	897	18.8	657	2	Q9NTV4	Q9NTV4 homo sapien
38	845.5	17.7	576	2	Q9HB46	Q9HB46 homo sapien
39	841.5	17.6	581	2	Q8VID8	Q8VID8 rattus norv
40	819.5	17.1	854	1	CNRB_HUMAN	P35913 homo sapien
41	803.5	16.8	865	1	CNSA_CANFA	O77746 canis famil
42	801	16.8	875	1	CNSA_HUMAN	O76074 bos sapien
43	799.5	16.7	853	1	CNRB_BOVIN	P23439 bos taurus
44	799.5	16.7	862	1	CNRC_CHICK	P52731 gallus gall
45	797	16.7	856	1	CNRB_CANFA	P33726 canis famil

ALIGNMENTS

RESULT 1
ID CN2A_BOVIN STANDARD; PRT; 921 AA.
AC P14099; Q28064;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).
GN Name=PDE2A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomati;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A1).
RX MEDLINE=91373395; PubMed=1654333;
RA Sonnenburg W.K., Mullaney P.J., Beavo J.A.;
RT "Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase cDNA. Identification and distribution of isozyme variants".
RT J. Biol. Chem. 266:17655-17661 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).
RX TISSUE=Brain;
RA Juilfs D.M., Sonnenburg W.K., Seraji S., Beavo J.A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 592-921 FROM N.A.
RX TISSUE=Heart;
RA Je Trong H., Beier N., Sonnenburg W.K., Stroop S.D., Walsh K.A., Beavo J.A., Charbonneau H.;
RT "Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiesterase from bovine heart".
RL Biochemistry 29:10280-10288 (1990).
RN [4]
RP SEQUENCE OF 613-694 AND 808-868.
RX TISSUE=Heart;
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;
RT "Identification of a conserved domain among cyclic nucleotide phosphodiesterases from diverse species".
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312 (1986).
CC -1- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O = nucleoside 5'-phosphate.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=PDE2A1;

CC IsoId=O00408-2; Sequence=Not described;
CC Name=PDE2A;
CC IsoId=O00408-3; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: Expressed in brain and to a lesser extent in
CC heart, placenta, lung, skeletal muscle, kidney and pancreas.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -!- SIMILARITY: Contains 1 GAF domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U67733; AAC51320.1; --
CC Genew; HGNC:8777; PDE2A.
CC MIM; 602658; --
CC GO; GO:0004118; P:cGMP-stimulated cyclic-nucleotide phosphodi. .; TAS.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; Met_phos_hydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF01590; GAF; 2.
CC PRINTS; PR00387; PDIESTRASE1.
CC SMART; SM0065; GAF; 2.
CC SMART; SM00471; HDC; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
KW Alternative splicing; cGMP; Hydrolyase; Membrane.
FT DOMAIN 372 550
FT DOMAIN 633 891 Catalytic (By similarity).
SQ SEQUENCE 941 AA; 105716 MW; 9797609B487FD64E CRC64;

Query Match 93.6%; Score 4474.5; DB 1; Length 941;
Best Local Similarity 94.7%; Pred. No. 3.5e-260;
Matches 860; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 14 QBPVPPGSDGALQDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTLIDGSRSLVC 73
DB 35 EPPPPPPQPCADSLQDALLSLGSDVIDSLQRAVKALSAVLPRVETVYTLIDGSRSLVC 94
QY 74 EBPPELPEQGVKREAVISRKELGCGNLGSPDLPKPLARLVAFLAPDTQVLVPLVDKE 133
DB 95 EBPPELPEQGVKREAVISRKELGCGNLGSPDLPKPLARLVAFLAPDTQVLVPLVDKE 154
QY 134 AGAAVAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQORESSVAPETQNPPEAA 193
DB 155 AGAAVAVILVHCGQLSDNEENSLQAVEKHTLVALKRVQALQORESSVAPETQNPPEAA 214
QY 194 GQKGGVAVTNDKTLQCGELXDLDASSLQQLKVLQYLQQTQASRCCLLVSDNLQL 253
DB 215 EDQKGAAYTDRDKLQCGELXDLDASSLQQLKVLQYLQQTQASRCCLLVSDNLQL 274
QY 254 SKCVIGDKVLEBEI SPPTTTGRIGQGVVEDKSIQLKDLTSDMQQLQSMGCEVQAMLCV 313
DB 275 SKCVIGDKVLEBEI SPPTTTGRIGQGVVEDKSIQLKDLTSDMQQLQSMGCEVQAMLCV 333
QY 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLSTLAFQKEQLKCEC 373
DB 334 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTYSTVLSTLAFQKEQLKCEC 393
QY 374 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAETCSVFLDDQNLVAKVDPGGVDE 433
DB 394 QALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAETCSVFLDDQNLVAKVDPGGVDE 453
QY 434 SYEIRIPADQGIAGHVAITGQILNIPDAYAHPFLYRGVDDSTGTFRTNLCPIKNEQ 493
DB 454 SYEIRIPADQGIAGHVAITGQILNIPDAYAHPFLYRGVDDSTGTFRTNLCPIKNEQ 513
QY 494 VTGVAELVNKINGPWFSPKFEDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553

DB 514 VTGVAELVNKINGPWFSPKFEDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 573
QY 554 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALSLQDMNFNNYK 613
DB 574 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALSLQDMNFNNYK 633
QY 614 IDCPILARFCLMVKGYRDPYHNNWHAHSVHFCVLLYKNELTNYLEDMEIFALFISC 673
DB 634 IDCPILARFCLMVKGYRDPYHNNWHAHSVHFCVLLYKNELTNYLEDMEIFALFISC 693
QY 674 MCHDLDRHTNNSFVASKSVLAALYSSEGSVWERHHPAQAIATLNTGHCNIFDHF SRKD 733
DB 694 MCHDLDRHTNNSFVASKSVLAALYSSEGSVWERHHPAQAIATLNTGHCNIFDHF SRKD 753
QY 734 YQRMDLMDRIILATDLAHLRFKDLQKMAEYGVDRNTKQHSLLCLLMTSCDLSQDT 793
DB 754 YQRMDLMDRIILATDLAHLRFKDLQKMAEYGVDRNTKQHSLLCLLMTSCDLSQDT 813
QY 794 KGWKTRKIAELIYKEFFSQGLEKAMGNRPNEMDMREKAYIPELOISPMHIAMPIYKL 853
DB 814 KGWKTRKIAELIYKEFFSQGLEKAMGNRPNEMDMREKAYIPELOISPMHIAMPIYKL 873
QY 854 LODLPKAAELYERVASNRHWTKVSHKFTIRGLSNNSLDFLDEYEVDPDLDGARAPIN 913
DB 874 LODLPKAAELYERVASNRHWTKVSHKFTIRGLSNNSLDFLDEYEVDPDLDGARAPIN 933
QY 914 GCCSLDAE 921
DB 934 GCCSLDAE 941

RESULT 3
Q8IW54 PRELIMINARY; PRT; 941 AA.
AC Q8IW54;
DT 01-WAR-2003 (TRENBLrel. 23, Created)
DT 01-WAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE Phosphodiesterase 2A, cGMP-stimulated.
GN Name=PDE2A;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haigh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

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CC -----
CC EMBL; BC006845; AAH06845.1; -;
CC DR EMBL; BC029810; AAH29810.1; -;
CC DR EMBL; BC057029; -; NOT_ANNOTATED_CDS.
CC DR PDB; 1MCO; X-ray; -;
CC DR MGD; MGI:2446107; Pde2a.
CC DR InterPro; IPR002073; PDease.
CC DR Pfam; PF00233; PDease_1; 1.
CC DR PRINTS; PRO0387; PDISTESTERASE1.
CC DR PROSITE; PS00126; PDEASE_1; 1.
CC KW 3D-structure; cGMP, Hydrolase; Membrane.
CC FT DOMAIN 348 526 GAP.
CC FT DOMAIN 609 867 Catalytic (By similarity).
CC FT SITE 421 422 GMP binding.
CC FT BINDING 407 407 GMP.
CC SQ SEQUENCE 916 AA; 103287 MW; 51C03B086633BF20 CRC64;

Query Match 92.6%; Score 4426; DB 1; Length 916;
Best Local Similarity 92.1%; Pred. No. 2.7e-257;
Matches 846; Conservative 35; Mismatches 34; Indels 4; Gaps 1;

QY 1 MRRQPAASRDPAQEPVPPSGDGLQDALLSGVIVAGLQQAQVKEALSAPLKVETV 60
DB 1 MRRQPAASQDPLAQKPEPPSGDRDLLEDALLSGAVIDLAGLQAARDALSAPLKVETV 60

QY 61 YTYLLDGESRLVCEPPELPOGKREAVISGRKLCNGLGSPDLPGKPLARLAPLAP 120
DB 61 YTYLLDGESRLVCEPPELPOGKREAVISGRKLCNGLGSPDLPGKPLARLAPLAP 120

QY 121 DTQVLVPLVDKAGAAVAVILVHCQSLDNEFSLQAVEKHTLVALKRVQALQRESSV 180
DB 121 DMQVLVPLLDKETSVAAILVHCQSLDSEESLQVVEKHALVALRRVQALQRR--- 177

QY 181 APEATONPPEAAGDQGGVATVNDQRKILQCGELYLDLASSLQKVLQYLOQETQASR 240
DB 178 -PEAVQNTSVSDASEQDKSGYTDHDKILQCGELFDLDATSLQKVLQYLOQETQATH 236

QY 241 CCLLVSEDLQSLCKVIGDKVLEERISPLTTGRLGVQVEDKSKLQKLDLSEDMQQLQ 300
DB 237 CCLLVSEDLQSLCKVIGDKVLEEVSPFLTNGRLGVQVEDKQCIQLKDLTSDVQQLQ 296

QY 301 SMLGCEVQAMLCVPVISRATDQVALACAFNKLGGDLFTDDEHVIQHFYHTSTVLST 360
DB 297 NMLGCELQAMLCVPVISRATDQVALACAFNKLGGDFFTDEHVIQHFYHTGVLST 356

QY 361 LAFQKEQKLCBQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 420
DB 357 LAFQKEQKLCBQALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLLDQNEL 416

QY 421 VAKVFDGGVDESEIIRIPADQGIAGHVATTGQILNIPDAYAHLPLFRGVDDSTGFRTR 480
DB 417 VAKVFDGGVDDSEIIRIPADQGIAGHVATTGQILNIPDAYAHLPLFRGVDDSTGFRTR 476

QY 481 NLICFPKINENQEVGVAEVLNKNPFSKEDDLATAFISYCGISIAHSLLYKKVNEA 540
DB 477 NLICFPKINENQEVGVAEVLNKNPFSKEDDLATAFISYCGISIAHSLLYKKVNEA 536

QY 541 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAADSNFASFTYTPRSLPEDDTSMAIL 600
DB 537 QYRSHLANEMMYHMKVSDEYTKLLHDGIQPVAADSNFANFTYTPRSLPEDDTSMAIL 596

QY 601 SMLQDMFNNTYKIDCPTLARCLMVKGYRDPFPHNMHAFSVSHFCVLLYKNLELTY 660
DB 597 SMLQDMFNNTYKIDCPTLARCLMVKGYRDPFPHNMHAFSVSHFCVLLYKNLELSNY 656

QY 661 LEDMEIPALFISCMCHDLDRGTNNSFQVASKSVLAALYSRSGSVYMERHHPAQATAINT 720
DB 657 LEDIEIPALFISCMCHDLDRGTNNSFQVASKSVLAALYSRSGSVYMERHHPAQATAINT 716

QY 721 HGCNIFDHFPSRKYQRMULDMDRIITLATDLAHLIRIFKDLQKMAEYGVYDNNRQHRLLL 776
QY 781 CLLMTSCDLSQDTGKWKTKRKAELIYKEFFSQGDLKAMGNRPMMEMDREKAYIPELQI 840
DB 777 CLLMTSCDLSQDTGKWKTKRKAELIYKEFFSQGDLKAMGNRPMMEMDREKAYIPELQI 836

QY 841 SEMEHIAPIYKLLQDLPPKAAELYERVASNEHHTKVKSHKFTIRGLPSNNSLDPLDEEY 900
DB 837 SEMEHIAPIYKLLQDLPPKAAELYERVASNEHHTKVKSHKFTIRGLPSNNSLDPLDEEY 896

QY 901 EYVDDLGGARAPINGCCSLD 919
DB 897 EYVDDLGGARAPINGCCSLD 915

RESULT 5
CN2A RAT STANDARD; PRT; 928 AA.
ID CN2A RAT Q01062;
AC Q01062;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).
DE Name=Pde2a;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=95110334; PubMed=7811274;
RA Yang Q., Paskind M., Bolger G., Thompson W.J., Repaske D.R.,
RA Cutler L.S., Epstein P.M.;
RT "A novel cyclic GMP stimulated phosphodiesterase from rat brain.";
RL Biochem. Biophys. Res. Commun. 205:1850-1858(1994).
RN [2]
RP SEQUENCE OF 643-759 FROM N.A.
RX MEDLINE=92406782; PubMed=1326532;
RA Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;
RT "A polymerase chain reaction strategy to identify and clone cyclic
nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA
encoding the 63-kDa calmodulin-dependent phosphodiesterase.";
RL J. Biol. Chem. 267:18683-18688(1992).
CC -!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
CC nucleoside 5'-phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=PDE2A3;
CC IsoId=Q01062-1; Sequence=Displayed;
CC Name=PDE2A1;
CC IsoId=Q01062-2; Sequence=Not described;
CC Name=PDE2A2;
CC IsoId=Q01062-3; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -!- SIMILARITY: Contains 1 GAP domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

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DR EMBL; U21101; AAA63683.1; -.
DR EMBL; M94540; AAA40922.1; -.
DR PIR; JC2486; JC2486.
DR RGD; 620965; pde2a.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 3.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Alternative splicing; cGMP; Hydrolase; Membrane.
FT DOMAIN 360 538
FT DOMAIN 621 879
FT CONFLICT 646 646 W -> R (in Ref. 2).
FT CONFLICT 758 758 L -> M (in Ref. 2).
SQ SEQUENCE 928 AA; 104663 MW; EF0B8C1E266EAB18 CRC64;

Query Match 90.5%; Score 4324.5; DB 1; Length 928;
Best Local Similarity 91.7%; Pred. No. 3.5e-251;
Matches 830; Conservative 32; Mismatches 38; Indels 5; Gaps 2;

QY 15 EPPVPPGSGDQALQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLVCE 74
DB 28 EPPVPPCAD-SLQDALLSLGAVIDIAGLRQAQDALSAVLPKVTYVTVYLLDGSRLVCE 86
QY 75 EPPHELPOEGKVREAVISRKLGCNGLGSPDLPGKPLARLVAPLADPTQVLVPLVDKEA 134
DB 87 DPPHELPOEGKIREAVISRKLSCDGLGSPDLLGKPLARLVAPLADPTQVLVPLLDKET 146
QY 135 GAVAAVILVHCGQLSDNEEWSLQAVEKTLVALKRVQALQRESVAPRATQNPPEAAG 194
DB 147 GTVAAVILVHCGQLSDSEESQLVVEKHALVALQVQALQRR----PEAVQNTSADPSE 202
QY 195 DQKGVAYTNDKRTLOLCGELYDLDASSLQQLKVLQYQQEQTQASRCCLLLVSDNLIQLS 254
DB 203 DQKEGYTAHDRKILQLCGELYDLDASSLQQLKVLRYLQQEQTQATHCCLLLVSDNLIQLS 262
QY 255 CKVIGDKVLEBEISPLTTRGLGVVEDDKSIQLKDLTSEDMMQQLQSMGLCEVQAMLCVP 314
DB 263 CKVIGEKVLGEVSPPLTMGRLGQVVEDKQCIQLKDLTSDVQQLQNMGLCGLRAMLCVP 322
QY 315 VISRATDQVVALACAFNKLGDGLFTDQDEHVIQHCFTHTSTVLSTLAFQEQKLKCECQ 374
DB 323 VISRATDQVVALACAFNKLGDGLFTDQDERAIOHCFTHTGTVLSTLAFQEQKLKCECQ 382
QY 375 ALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEITCSVFLDDQNELVAKVFDGGVDEES 434
DB 383 ALLQVAKNLFTHLDDVSVLLQEIITEARNLSNAEITCSVFLDDQNELVAKVFDGGVDDDES 442
QY 435 YEIRIPADQGIAGHVATTGQILNPIDAYAHPLFYRGVDDSTGFRTRNLICFPKINQEV 494
DB 443 YEIRIPADQGIAGHVATTGQILNPIDAYAHPLFYRGVDDSTGFRTRNLICFPKINQEV 502
QY 495 IGVAEVLNKGWPFKPEDLATAFYSYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 554
DB 503 IGVAEVLNKGWPFKPEDLATAFYSYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 562
QY 555 MKVSDDEVTKLLHDIQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMQDMNFINNYKI 614
DB 563 MKVSDDEVTKLLHDIQIPVAAIDSNFANFTYTPRSLPEDDTSMALLSMQDMNFINNYKI 622
QY 615 DCPTLARFCLMVKGYRPPYHNMWAFSVSHFCYLLYKNLELNTLYLDEMBEIPALFISCM 674
DB 623 DCPTLARFCLMVKGYRPPYHNMWAFSVSHFCYLLYKNLELNTLYLDEMBEIPALFISCM 682
QY 675 CHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIATLNTHCNIFDHFSCRKY 734
DB 683 CHDLDRGTNNSFQVASKSVLAALYSSEGSVMERHHPAQAIATLNTHCNIFDHFSCRKY 742
QY 735 QRMLDLMRDIIATDLAHLRI FKDLQKMAEVGYDRNTKQHSLLCLLMTSCDLSQDTK 794
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Db 743 QRMLDLMRDIIATDLAHLRI FKDLQKMAEVGYDRNTKQHSLLCLLMTSCDLSQDTK 802
QY 795 GWKTRTKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQISPMEHAMPIYKLL 854
DB 803 GWKTRTKIAELIYKEFFSQGDLKAMGNRPMMMDREKAYIPELQISPMEHAMPIYKLL 862
QY 855 QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDLDEEYEVDPDLGAPAPNG 914
DB 863 QDLFPKAAELYERVASNREHWTKVSHKFTIRGLPSNNSLDLDEEYEVDPDLVTRAPVNG 922
QY 915 CCSLD 919
DB 923 CCSLE 927

RESULT 6
Q6ZMR1
ID Q6ZMR1 PRELIMINARY; PRT; 685 AA.
AC Q6ZMR1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ16750.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSU=Adrenal gland;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK131525; BA018664.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 685 AA; 78177 MW; A6087394B98221C3 CRC64;

Query Match 67.5%; Score 3229; DB 2; Length 685;
Best Local Similarity 70.2%; Pred. No. 1.6e-185;
Matches 637; Conservative 11; Mismatches 10; Indels 250; Gaps 1;

QY 14 QEPVPPGSGDQALQDALLSLGSLVDVAGLQQAQKAEALSAVLPKVTYVTVYLLDGSRLV 73
DB 28 EPPVPPPCADSLQDALLSLGSLVDISGLQRAQKAEALSAVLPKVTYVTVYLLDGSRLV 87
QY 74 EEPHELPOEGKVREAVISRKLGCNGLGSPDLPGKPLARLVAPLADPTQVLVPLVDKE 133
DB 88 EDPHELPOEGKVR----- 101
QY 134 AGAAVAILVHCGQLSDNEEWSLQAVEKTLVALKRVQALQRESVAPRATQNPPEAA 193
DB 102 ----- 101
QY 194 GDQKGVAYTNDKRTKILQCGELYDLDASSLQQLKVLQYQQEQTQASRCCLLLVSDNLIQL 253
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Db 102 ----- 101
Qy 254 SKVIGDKVLEEISFPLTTGRLGQVVDKKSILQKLTSDMQOOLGMLGCEVQAMLCV 313
Db 102 ----- 101
Qy 314 PVISRATQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVTLTSTLAFQEKQKKEC 373
Db 102 -----FTDQDEHVIQHCFTYTVTLTSTLAFQEKQKKEC 137
Qy 374 QALLQVAKNLFTHLDVSVLLQEIITEARNISNAEICSVELLDQNELVAKVDFGQVWDE 433
Db 138 QALLQVAKNLFTHLDVSVLLQEIITEARNISNAEICSVELLDQNELVAKVDFGQVWDE 197
Qy 434 SYEIRIPADQGIAGHVAATGQILNIPDAYHPLFYRGVDDSTGFRNLCFFPIKNQOE 493
Db 198 SYEIRIPADQGIAGHVAATGQILNIPDAYHPLFYRGVDDSTGFRNLCFFPIKNQOE 257
Qy 494 VIGVAVELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 553
Db 258 VIGVAVELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMY 317
Qy 554 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTVPESLPEDDTSMALLSMLODMNFINNYK 613
Db 318 HMKVSDDEYTKLLHDGIQVAAIDSNFASFTVPESLPEDDTSMALLSMLODMNFINNYK 377
Qy 614 IDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFALFISC 673
Db 378 IDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFALFISC 437
Qy 674 MCHLDHRTGNNFSFOVASKSVLAALYSSEGVSWMERHHPAQAIILNTHGNCNIFDHSRKD 733
Db 438 MCHLDHRTGNNFSFOVASKSVLAALYSSEGVSWMERHHPAQAIILNTHGNCNIFDHSRKD 497
Qy 734 YQRMLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNKHSHLLCLLMTSCDLSDOT 793
Db 498 YQRMLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNKHSHLLCLLMTSCDLSDOT 557
Qy 794 KGWTKTRKIAELIYKEFFSQDLEKAMGNRPWEMMDREKAYIPELQISFMEHIAMPIYKL 853
Db 558 KGWTKTRKIAELIYKEFFSQDLEKAMGNRPWEMMDREKAYIPELQISFMEHIAMPIYKL 617
Qy 854 LODLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLOFLDEEYVDPDLDGARAPIN 913
Db 618 LODLFPKAAELYERVASNRHWTKVSHKFTIRGLPNSNSLOFLDEEYVDPDLDGARAPIN 677
Qy 914 GCCSLDAE 921
Db 678 GCCSLDAE 685

RESULT 7
ID096076 PRELIMINARY; PRT; 819 AA.
AC 096076;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE EFPDE2.
OS Ephydatia fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OX Haploeclerida; Spongillidae; Ephydatia.
NCBI TaxID=31330;
RN [1]_TaxID=31330;
RP SEQUENCE FROM N.A.
RX MEDLINE=99015760; PubMed=9801141; DOI=10.1016/S0014-5793(98)01150-8;
RA Koyanagi M., Suga H., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RT "Ancient gene duplication and domain shuffling in the animal cyclic
nucleotide phosphodiesterase family.";
RL FEBS Lett. 436:323-328(1998).
DR EMBL; AB017022; BAA34308.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2. 1.
DR Pfam; PF00233; PDEase_1; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM0065; GAF; 2.
DR SMART; SM00471; HGC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR SEQUENCE 819 AA; 92145 MW; F4CALEE8B23A9E0E CRC64;
Query Match 34.7%; Score 1661; DB 2; Length 819;
Best Local Similarity 39.9%; Pred. NO. 3.5e-91;
Matches 346; Conservative 161; Mismatches 256; Indels 104; Gaps 10;
Qy 27 QDALLSGSVLDVAGLQOAVKEALSAPLKVETVTVYLLDGESRLVC---EPPHEPQ 82
Db 23 EDALIGMAANSPTEFTAAAGCLRFTFSSAGVALLDTENNELAYFEENDKTHLPK 82
Qy 83 EGVREAVISRKRLGCGNLGSPDLPGKPLARLAPLAPDTQVLVPLVDKEAGAAVIL 142
Db 83 MGVVDAVRQR----- 93
Qy 143 VHCQQLSDNEWSLOAVEKHTLVALKRVOALQORESSVAPRATQNPBEAAGDQGGVAY 202
Db 94 ---TLEENYE-RLRLLERTTLVAAKRV-----LAH 119
Qy 203 TNQBRK-----ILQCGELYDLDAASSLQKVLQVLOQETOASRCCLLVSEDNQLQSK 256
Db 120 LNSEHEKRIIDNMLRVCGELIDLVVLSIKLKHIMEVSNAKACTLFVYEDVTQELVAY 179
Qy 257 VIGDKVLEEISFPLTTGRLGQVVDKKSILQKLTSDMQ---OLQSMLGCEVQAMLCV 313
Db 180 TYNGVPLDKETRPVSSSIYCEPTTGELINISV-PQDMRFPNPRIDIKGVEPTHLICI 238
Qy 314 PVISR---ATDQVVALACAFNKLGGDLFTDQDEHVIQHCFTYTVTLTSTLAFQEKQK 370
Db 239 PVKORGAGQSQSVGLVVCNDKNDRPFTKDEEGLYSLHFCSSMLNANTLVYQRELAK 298
Qy 371 CECQALLQVAKNLFTHLDVSVLLQEIITEARNISNAEICSVELLD---QNELVAKVDFG 428
Db 299 KQNEVLLQVAKNLFTHLDVSVLLQEIITEARNISNAEICSVELLDKRSNLVAVTFNGD 358
Qy 429 VVEDESVEIRPADQGIAGHVAATGQILNIPDAYHPLFYRGVDDSTGFRNLCFFPIK 488
Db 359 VLKERTLIKV--GGIAGYVAKGTIVNIYDAQKHPQFAEVDKSTGFTGTHLCFFPI 416
Qy 489 NENQEVIGVAVELVKNKINGPWFSPFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLAN 548
Db 417 DNGGVVGVAVELCNKINGKFTKYDEELARTFSAICYGISIVHSKLYETVMASQGRSLAT 476
Qy 549 EMMYHMKVSDDEYTKLLHDGIQVAAIDSNFASFTVPESLPEDDTSMALLSMLODMN 608
Db 477 ELMLYHKIRPDELERATKTPLPVSSPHEMCKLTFPSLDIKNSADEIAVNMNMNDL 536
Qy 609 INNVKIDCPTLAFCLMVKKGYRDPYPHNMWHAFFSVSHFCYLLYKNELTNYLEDMEIFA 668
Db 537 INKFQLHPDILARFVIMVKGTRDPPYHNMWHAFFSVHFLYALYCCSSKLSCLDLEVLA 596
Qy 669 LFISCMCHDLDRHGTGNNFSFOVASKSVLAALYSSEGVSWMERHHPAQAIILNTHGNCNIFD 728
Db 597 LFVSLCHDIDHRTGNNFQVCSNSTLACYSSSEGVSWMERHHLAQLTCLNSPGNCIFEN 656
Qy 729 FSRKDYQRMLDLMDRIILATDLAHLRIKDLQKMAEVGYDRNKHSHLLCLLMTSCD 788
Db 657 LSDSDYRTTIQLIQNDILDTDIASHLKKLKHIKQMANDGYERSNPEHRLMCSLMTSCD 716
Qy 789 LSDQTKGWTKTRKIAELIYKEFFSQDLEKAMGNRPWEMMDREKAYIPELQISFMEHIAM 848
Db 717 LTASCKTWESNKASDILIYQEFFSQDLEKALGVTPSEMMORDRAFIPEQQQLDNIAG 776

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Qy 849 PIYKLODLFPKAAELYERVASNEHW 875
Db 777 FVYQLSLRPESAAAHVTLIDNREQW 803

RESULT 8
Q7Q4A0
ID Q7Q4A0 PRELIMINARY; PRT; 491 AA.
AC Q7Q4A0 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EbiP6713 (Fragment)
GN Name=ebiG6713; ORFNames=ENSANGG00000005075;
OS Anopheles gambiae str. FEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008964; EAA12229.1; -.
DR GO; GO:0004114; F:3, 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR PROSITE; PS00126; PDEASE_I; 1.
FT NON_TER 1
FT NON_TER 491
SQ SEQUENCE 491 AA; 56349 MW; 54161322CE42EF3 CRC64;

Query Match 25.9%; Score 1236; DB 2; Length 491;
Best Local Similarity 50.5%; Pred. No. 5.8e-66;
Matches 250; Conservative 91; Mismatches 138; Indels 16; Gaps 8;

Qy 393 LQIIEITARNLSNAETCSVFLDQ--ELVAKVFDGQVDESEYETRIPADQGIAGHVA 450
Db 4 LLRGVMTAEKELAAARCSFLDKHTGELVSKVFDG---NEASKEIRIESGKGAGYVA 60

451 TTGQILNIPDAYAHPFLYRGVDDSTGFRTRNLCPPIKNENQEVIGVAELVNKINGPWS 510
Db 61 QTGKLLNIRNAYQHPLFYKGVDESTGFKTRNLCPPICDE--EGVIGVAQLCNKNGHFHD 119

511 KFDDELATAFYCGISIAHSLLYKYVNEAQYRHLANEMMYHMKVSDDEYTKLLHDGI 570
Db 120 KCDEVATAFSVYCGISIMHALVHKVQKAEARKYLSQELLLYHMKVDPDTEVNALEAVK 179

571 QPVAADIS--NFASTYTPPSLPEDDTSMAL--LSMLQDMFNINNYKIDCPTLPARCLMV 626
Db 180 EPDREQDELTYTFRFPFCPRDVKDHALSVQLAMRMFYDLNFVSGFKIHEYKLFARFVLV 239

627 KKGVRDPYNNMHAFSVSHCYLLYKNLEL--TNYLEDMEIFALFSCMCHDLDRGTN 684
Db 240 QKGYRDPYNNMHAFSVAHFAYSLMNNLRIRERGITKMGQGFSLTAAPCHDLDRHGIS 299

685 NSFVASKSVLAALYSSEGSVMERHFAQAIALNTHGNCNFDHFSKDYQRMULDLMRDI 744
Db 300 NSYQTSSPLARYSSEGSVMERHLSQAICILNDSSSKLDGLSTFEKECIDYLREL 359

745 ILATDLAHLHIFKDLQKM--AEVGVDRTNKQHSLLLCLLMTSCDLSQTKGKWTTRKIA 803
Db 360 ILATDLANHFRILPRLKRLAEYLTEGNSQR---LLLSLMTTCDDLNDQIKSWKTQHVVA 416

804 ELIYKEPFGDLKACMGNRMWMDREKAVIPELOISFMHEIAMPYIKLQDLPPRAAE 863
Db 797 RSLICMAIKNSLQIIGVLIQILINKFNELDTFKNDENFVEAFICGMGIHNTMYEKAIV 856

Db 417 HLVVAEPPFAEGDLEKQMLRPNAMMDRKKACIPMLQIEFLTTVIRTPFEILVQIFPETGS 476
Qy 864 LYERVASNREHWTKV 878
Db 477 FLDTIDSNRREQW 491

RESULT 9
Q8MQW0
ID Q8MQW0 PRELIMINARY; PRT; 1544 AA.
AC Q8MQW0 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SUI3096p.
GN Name=Pdel1; Synonyms=CG10231;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbavani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacble J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY122262; AAM52774.1; -.
DR FlyBase; FBgn0032686; Pdel1.
DR GO; GO:0004114; F:3, 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 1544 AA; 171689 MW; F525480CCDB3D065 CRC64;

Query Match 20.7%; Score 992; DB 2; Length 1544;
Best Local Similarity 32.2%; Pred. No. 1.4e-50;
Matches 245; Conservative 147; Mismatches 302; Indels 68; Gaps 19;

Qy 209 ILQCGELYDLDASSLQKLVLYLQQTQASRCCLLLV-----SEDNLQLSKV----- 257
Db 502 VKDICNE--LEVRTLCHKILQNVISILLNADRGSLFVQGRCNPGDLK-KCLVSKLFDV 557

258 -----IGDKVLEERISFPLTTLGRLGQVVEDKKS1QLKDLTSEDN--QOLQSLMGEVQAM 310
Db 558 CPRSTVEEMSQDDSVRVAVGTGIAGHVAESGEPNIPDAYODERFNCIDSLTGRYTKAL 617

311 LCVFVISRATDQVVALACAFNKLGGDLFTDDEHVIQCHFTYTSVLTSTTLAFOKEQKLK 370
Db 618 LCPKIDSSGD-VIGVAQVINKNKGECFSEIDEKVFSYLOFCGIGLRNAQLYKESQLEI 676

371 CEQALLQVAKNLPHTLDDSVLLQEIITEARNLSNAEICSVFLDDQNE--LVAKVFD-- 426
Db 677 KRNVQLDLARMIPEEQSTIEHVMFRILTHMQSLIQCORVQILLVHEADKGSFRVDFE 736

427 -GGVVEDS-----YEIRPADOGIAGHVATTCCQILNIPDAYAHPFYRGVDDSTGPR 479
Db 737 ANDLSEBEARTSPYSRPFINGITGHVATTGVTWVNPVAYEDDPADSVSDNSCFKH 796

480 RNILCFPIKNNENQEVIGVAELVNKINGPWSFKPDDELATAFSIYCGISIAHSLLYKYVNE 539
Db 797 RSLICMAIKNSLQIIGVLIQILINKFNELDTFKNDENFVEAFICGMGIHNTMYEKAIV 856
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Db 831 AELVTSEFFEQDRERLEKLTPSAIPDRNRKDELPRQLQLEWIDSICMPLYQALVKVNVK 890
Qy 861 AELYERVASNREHWTKVSHKFTTIGLPSNNS 892
Db 891 LKPMLDVSATNRKWEELHQLRLASTASSSS 922

RESULT 11
Q96S76 PRELIMINARY; PRT; 988 AA.
ID Q96S76;
AC Q96S76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11121118;
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanoh Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene;
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1; -.
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
DR EMBL; AB048408; BAB62713.1; JOINED.
DR EMBL; AB048409; BAB62713.1; JOINED.
DR EMBL; AB048410; BAB62713.1; JOINED.
DR EMBL; AB048411; BAB62713.1; JOINED.
DR EMBL; AB048412; BAB62713.1; JOINED.
DR EMBL; AB048413; BAB62713.1; JOINED.
DR EMBL; AB048414; BAB62713.1; JOINED.
DR EMBL; AB048415; BAB62713.1; JOINED.
DR EMBL; AB048416; BAB62713.1; JOINED.
DR EMBL; AB048417; BAB62713.1; JOINED.
DR EMBL; AB048418; BAB62713.1; JOINED.
DR EMBL; AB048419; BAB62713.1; JOINED.
DR EMBL; AB048420; BAB62713.1; JOINED.
DR EMBL; AB048421; BAB62713.1; JOINED.
DR EMBL; AB048422; BAB62713.1; JOINED.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 988 AA; 111169 MW; 7F678869353DF7BB CRC64;

Query Match 20.7%; Score 991; DB 2; Length 988;
Best Local Similarity 30.8%; Pred. No. 8.4e-51;
Matches 250; Conservative 159; Mismatches 321; Indels 82; Gaps 19;

Qy 143 VHCGLSDNBSWSLQAVSKHTLVAKRVAQLQORESSVAP-----EATQNPPS-- 190
Db 185 IHWRTYD-EQVTSRAQEP LSV---RRRLRKASSLPPTAHLISALLSRVNLQYP 240
Qy 191 EAAGDQKGGVAYTNQDRKILQCGEL-VYLDASSLQLKVLQYLOQETOASRCCLLLVSED 249
Db 241 PTADYKCHLKXKHNQRQFFLELVKDISNDLDTLSYKILIFVCLMWADVADRCSLFLV--E 298
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RESULT 12

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Q95TW8 PRELIMINARY; PRT; 1018 AA.
ID Q95TW8
AC Q95TW8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH27433p.
GN Name=Pde6; Synonyms=CG8279;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Paciel J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celnik S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AY058470; AAL13699.1; -.
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RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
EX MEDLINE-22426065; PubMed-12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
EX MEDLINE-22426070; PubMed-12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.,
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
EX MEDLINE-22426069; PubMed-12537572;
RA Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.,
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003659; AAF3675.2; --
DR FlyBase; FBN0032686; Pdel1.
DR GO; GO:0004114; F3,5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_1; 1.

DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HGC; 1.
DR PROSITE; PS00126; PDEase I; 1.
SQ SEQUENCE 1365 AA; 151173 MW; B0562E2FDF5012E56 CRC64;
Query Match 20.6%; Score 983; DB 2; Length 1365;
Best Local Similarity 31.3%; Pred. No. 4.1e-50;
Matches 246; Conservative 147; Mismatches 303; Indels 90; Gaps 19;
QY 209 ILQCGELYDLDASSILQKLVLYLQYQEQTAQSCCLLV-----SENLQLSCKV----- 257
DB 299 VKDINCNE---LEVRTLCHKILQNVILLNADRGSLFLVQGRGNGPGLK-KCLVSKLFDV 354
QY 258 -----IGDKVLEEISFPLTTGRLGQVVEDKKSIOQLKDLTSDM--QQQLSMGLGCVQAM 310
DB 355 CPRSTVEEMEQQDEVRAVWGTTGIAGHVAESGEPVNPIDAYQDERFNCEDLSLTGYRTKAL 414
QY 311 LCVPIVRATDOVALACAFNKLGGDLFTDQDEHVIQCHFYHTVSTVLTSTLAFQKEOKLK 370
DB 415 LCMPIKDSGD-VIGVAQVINNMNGECFSEIDKRVFSSYLQFCGIGLRNAQLYKESQLEI 473
QY 371 CECQALLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVELLDONE--LVAKVFD-- 426
DB 474 KXQVLLDLARMIFEEQSTIEHNVPRILTHMQSLQCQVQLLVHEADKGSFVRVDFE 533
QY 427 -GGVVEDES-----YEIRPADQGIAGHVATTGQILNIPDAYAHLPLFYRGVDDSTGPR 479
DB 534 ANDLSEBATSRTSPYESRFPINIGITGHVATTGETVNVPNAYEDDRPDASVDENSCPKH 593
QY 480 RNILCFPIKNEQVIGVAELVNKNGPWFSEFDEDLATAPSIYCGISIAHSLLYKVNVE 539
DB 594 RSILCMAIKNSLGQIIGVIQILNKFNELDTKNDENFVEAFAPFCGMGIHNTMYEKATV 653
QY 540 AOYRSHLANEMMYHMKVSDDEYTKL-----LHDGIGPVAA 575
DB 654 AMAQSVTLVLSYHASATMDAHLRKQKQKQQAQVGLRQAPLSPPRKKLQRLRVP 713
QY 576 IDSNSPASYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKVKGYPDP 635
DB 714 VHFRLHDFKDDIHFDDEDDTLKACLRMFLDLDFVERPHIDYEVLCRWLLSVKKNYRNV 773
QY 636 HNWMAFVSVSHFCYLLYKNLELTNYLDMETPALFISCMCHDLDRGTNNSFQVASKSVL 695
DB 774 HNWRAFNVAQWMAFALTITQWKKIFGEICLALIGCLCHDLDRGTNNSFQIKASSPL 833
QY 696 AALYSSEGSVMERHFAQAIALINTHCNIIDHFSRKDYORMLDLMDRDIILATDLAHLR 755
DB 834 AOLYST--STWEHHFDCQLMILNSFGNQLANLSSDDYCRVIRVLEDDALLSTDLAVY-- 889
QY 756 IFKD----LQMAEYGYDRTNKKHSHLLCLLMTSCDLSDDQTKGKWTTRKIAELIYKEFF 911
DB 890 -FKKGGPFLSVSQPTSYVAEEPRALLRAMSMTVCDLSAITKPKWEIKRVADLVSEFF 948
QY 812 SQGDLEKAMGN-RPMEMMDREKA-YIPQLQTSFMEHIAMPIYKLLQDLFPKAAELYERVA 869
DB 949 EQGDMKQELNITPIDINREKEDLPMQVNFIDSLICLIPEAFATLSKLEPLVEGYR 1008
QY 870 SNREHW-----TKVS-----HKFTIRGLPSNNSL-----DFLDEEYVVP-DLDGA 908
DB 1009 DNRGHMIDLADVVKTKTSQDQEPPEEEQQQNVISNGDCKAMSDDDVAASEAVDPSPE 1068
QY 909 RAPING 914
DB 1069 KASVNG 1074
RESULT 15
QVID6
ID Q8VID6 PRELIMINARY; PRT; 935 AA.
AC Q8VID6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

QY 1 MRQPAASRDLPQAPVPPGSDGALQDALLSLGSDVIDVAGLQQAVALSAVLPGKVTY 60
Db 1 MRRQPAASRDLPQAPVPPGSDGALQDALLSLGSDVIDVAGLQQAVALSAVLPGKVTY 60
QY 61 YTYLLDGSRLVCEBPPHELPOEGKVRBAVTSRKELGCGNGLGPSDLPKPKLARLVAPLAP 120
Db 61 YTYLLDGSRLVCEBPPHELPOEGKVRBAVTSRKELGCGNGLGPSDLPKPKLARLVAPLAP 120
QY 121 DTQVLVILPLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
Db 121 DTQVLVILPLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSV 180
QY 181 APEATONPPEEAAGDQKGGVATNODRKILQCGELYDLDAASSLQKLVQVLOQETQASR 240
Db 181 APEATONPPEEAAGDQKGGVATNODRKILQCGELYDLDAASSLQKLVQVLOQETQASR 240
QY 241 CCLLVSEDNLQLSCKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDNQQLQ 300
Db 241 CCLLVSEDNLQLSCKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDNQQLQ 300
QY 301 SMLGCEVQAMLCVPIVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLST 360
Db 301 SMLGCEVQAMLCVPIVISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLST 360
QY 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420
Db 361 LAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNEL 420
QY 421 VAKVFDGGVVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
Db 421 VAKVFDGGVVEDESVEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTR 480
QY 481 NILCPPIKNEQEVTVGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEA 540
Db 481 NILCPPIKNEQEVTVGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEA 540
QY 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
Db 541 QYRSHLANEMMYHMKVSDDEVTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAIL 600
QY 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWAFSVSHFCYLLYKXLELNY 660
Db 601 SMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYPYHNMWAFSVSHFCYLLYKXLELNY 660
QY 661 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPFAQAIINT 720
Db 661 LEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPFAQAIINT 720
QY 721 HGCNIFDHFSRKDYORMLDLARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
Db 721 HGCNIFDHFSRKDYORMLDLARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLL 780
QY 781 CLMTSCDLSQDTKGWTKTRIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELQI 840
Db 781 CLMTSCDLSQDTKGWTKTRIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELQI 840
QY 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLSPNNSLDFLDEY 900
Db 841 SFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVSHKFTTIRGLSPNNSLDFLDEY 900
QY 901 EVPDLGAPINGCCSLDAE 921
Db 901 EVPDLGAPINGCCSLDAE 921

RESULT 2
JC2486
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat
N:Alternate names: cGMP-dependent phosphodiesterase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C/Accession: JC2486

R;Yang, Q.; Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein
Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994
A>Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.
A/Reference number: JC2486; MUID:95110334; PMID:7811274
A/Accession: JC2486
A/Molecule type: mRNA
A/Residues: 1-928 <YAN>
A/Cross-references: UNIPROT:Q01062; GB:U21101; NID:g706929; PIDN:AAA63683.1; PID:g706930
A/Experimental source: brain
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-
C;Keywords: alternative splicing; cAMP binding; cAMP binding; homodimer; phosphoprotein;
P:643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
P:109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 90.5%; Score 4324.5; DB 1; Length 928;
Best Local Similarity 91.7%; Pred. No. 1.4e-274;
Matches 830; Conservative 32; Mismatches 38; Indels 5; Gaps 2;
QY 15 BPVPPGSDGALQDALLSLGSDVIDVAGLQQAVALSAVLPGKVTYTYLLDGSRLVCE 74
Db 28 EPPQPCAD-SLQDALLSLGNAVIDIAGLRQAQKALSAVLPKVTYTYLLVDEGSRVCE 86
QY 75 BPPHELPOEGKVRBAVTSRKELGCGNGLGPSDLPKPKLARLVAPLAPDTQVLVILPLVDEA 134
Db 87 DPPHELPOEGKI REAVISRKELSCDGLGPSDLLGKPLARLVAPLAPDTQVLVILPLDKET 146
QY 135 GAVAAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPATONPPEEAAG 194
Db 147 GTVAAVILVHCGQLSDSEEQSLQVVEKHALVALQVQALQORR---PEAVQNTSADPSE 202
QY 195 DQKGGVATNODRKILQCGELYDLDAASSLQKLVQVLOQETQASRCLLVSEDNLQLS 254
Db 203 DQKDEKGYTAHDRKILQCGELYDLDAASSLQKLVRYLQETQATHTCCLLVSEDNLQLS 262
QY 255 CKVIGDKVLEEEISFPPLTTGRLGQVVEDKKSQIQKDLTSEDNQQLQSMGCEVQAMLCVP 314
Db 263 CKVIGDKVLEEEISFPPLTTGRLGQVVEDKQCIQKDLTSDVQQLQNMGLGCELRLMLCVP 322
QY 315 VISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQ 374
Db 323 VISRATQVVALACAFNKLGGDLFTDQDEHVIQCHFYTSTVLSTLAFQKEQKLKCEQ 382
QY 375 ALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDEES 434
Db 383 ALLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSVFLLDQNELVAKVFDGGVDDDES 442
QY 435 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCPPIKNEQEV 494
Db 443 YEIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSTGFRTRNILCPPIKNEQEV 502
QY 495 IGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 554
Db 503 IGVAELVNKINGPWFSPKDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYH 562
QY 555 MKVSDDEVTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMQDMNFNNYKI 614
Db 563 MKVSDDEVTKLLHDGIQPVAAIDSNFANFTYTPRSLPEDDTSMAILSMQDMNFNNYKI 622
QY 615 DCPTLARFCLMVKKGYRDPYPYHNMWAFSVSHFCYLLYKXLELNTLYLDEMEIFALFISCM 674
Db 623 DCPTLARFCLMVKKGYRDPYPYHNMWAFSVSHFCYLLYKXLELNTLYLDEMEIFALFISCM 682
QY 675 CHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPFAQAIILNTHGCNIFDHFSRKDY 734
Db 683 CHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHPFAQAIILNTHGCNIFDHFSRKDY 742
QY 735 QRMELDLARDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHSLLLCLMTSCDLSQDTK 794
Db 743 QRMELDLARDIILATDLAHLRIFKDLQKMAEVGYDRNNKQHRLLCLMTSCDLSQDTK 802
QY 795 GWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLL 854
Db 803 GWKTRKIAELIYKEFFSQGDEKAMGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLL 862

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

```
Query Match      16.7%; Score 799; DB 1; Length 856;
Best Local Similarity 26.5%; Pred. No. 4.2e-44;
Matches 223; Conservative 161; Mismatches 331; Indels 128; Gaps 24;

QY 189 PEENAGDQGG-----VAYTNQDKIKLQCGELYD-LDASSLQIKVLOYLQOETQ 237
DB 29 PEHVAGACDGOPTDCASFELCQVBEAALFELVQDMQESVNMERVVFKILRLCTILR 88
QY 238 ASRCCLLLVSDN--LQLSCKVIG--DKVLEE-----EISFPLTTGRLGOVVDKKS 285
DB 89 ADRCSLFWYRQNGVAELATRLFSVQPGSALEDCLVPPDSEIVFPDLIDIGVGHVATKKM 148
QY 286 IQLKDLTS--EDMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTDQDE 343
DB 149 VNVQDVTECPHFSPPADELGTGYETRNILATPIWN--GKEVAVIMALKNDLGGPCFTSEDE 206
QY 344 HVIQHCFHYTSTVLSTLAFQEKQKKEC---QALLQVAKNLFTHLDDVSVLLQELITE 400
DB 207 DVFP---LKYLNFGTLNLKTYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQHFAYT 263
QY 401 ARNLNSNAETCSVFLDDQNELVAKVFDGGVV---EDESY----- 435
DB 264 VYALNCDRYSVGLLDMTK-EKEFFDVWVPLMGEAQPSGPRTPDGREIVFVKVYDIILH 322
QY 436 ---EIRI-----PAD-----QGIAGHVATTGQILNPDAVAHPL--FYRGVDDSTGPR 481
DB 323 GKEDIKVIKIPSPADHWALASGLPTYVAESGFCINMTAADEMFTQEGPLDSDGVIK 382
QY 482 ILCFPIKQENQVIGVAELVNKINGPWSKFPEDLATAFSIYCGISIAHSLLYKKVNEAQ 541
DB 383 VLSMPTVKNKEBIVGATFYNRKDGKFPDQDEVLMEISLTQFLGWSVLNTDTYDKMKLE 442
QY 542 YRSHLANEMMYHMKVSDDEYTKLHD-----GIQPVAAATDSNFA----- 581
DB 443 NRKQIAQDMVLYHVRCDKDEIQILPTRRERLKEPADCEDELGILLKEVLPGSKFDIY 502
QY 582 SFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNWMA 641
DB 503 EPHPSDLECTELELVKCGIQMYVELGVVRKFQIPQEVLRFLFSVSKGYRRITYHNWRHG 562
QY 642 FSVSHFCYLLYKNLELTYNLEMEITAFIPISCMCHDLHRGTNNNSFQVASKSVLAALYSS 701
DB 563 FNAVQTMFTLLTATGKSYTDLFAFAMVTAGLCHDHRGTNNLYQMSQNPPLAKLHGS 622
QY 702 EGSVMERHHFAQAIALLNTHGNCNIPDHFSEKDYQRMLDLWRDILATDLAHLRIFKDLQ 761
DB 623 --SILRHHLEFGKFLSSEETLNIYQNLNRQHEHVHILMDIATDIALYFKKRTWFO 680
QY 762 KMAE-----VGDRTNKQHHSLLLCLMTSCDLSQDTKGWKTTRKIAELIYKEF 810
DB 681 KIVDESKNVEDRKSWEVYLSLETTKEIVWAMMTACDLSATKPEVQSKVALLVAEAF 740
QY 811 FSQGDLEK-AMGNRPMEHMDREK-AVYPELQISFMEHTAMPYIKXLQDLFPKAAELYERV 868
DB 741 WEQGLERTVLQDQPIPMNRNKAELPKLQVGFDFVCTFYVYKFSRPHSEILPMFDR 800
QY 869 ASNREHWTYKSHKPTIRGLPSNNSLDPLDEEVEVD-----LDGARAPING-C 915
DB 801 QNNRKEWALADEYEA-----LKALEBEKQOQEDRTTAKKAGTEICNGGPAKSTC 853
QY 916 CSL 918
DB 854 CIL 856
```

RESULT 10

S30762

3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 22-Nov-1993 #sequence revision 19-Oct-1995 #text_change 09-Jul-2004

C:Accession: S30762; S13031; S13121

R:Baehr, W.

submitted to the EMBL Data Library, June 1991

A:Reference number: S30762

A:Accession: S30762

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-856 <BA>

A:Cross-references: UNIPROT:P23440; EMBL:X60133; NID:G53595; PIDN:CAA42719.1; PID:G53596

R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittier, S.J.

FEBS Lett. 278, 107-114, 1991

A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha

cing of the beta-subunit gene

A:Reference number: S13030; MUID:91130581; PMID:1847109

A:Accession: S13031

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-559, 'G', 561-856 <BA2>

A:Cross-references: EMBL:X60133

R:Bowes, C.; Li, T.; Danciger, M.; Baxter, L.C.; Applebury, M.L.; Farber, D.B.

Nature 347, 677-680, 1990

A:Title: Retinal degeneration in the rd mouse is caused by a defect in the beta subunit

A:Reference number: S13121; MUID:91015387; PMID:1977087

A:Accession: S13121

A:Molecule type: mRNA

A:Residues: 1-2, 'X', 4, 'G', 6-18, 'S', 20-48, 'DV', 51-157, 'T', 159-175, 'C', 177-231, 'R', 233-235

A:Cross-references: EMBL:X55968; NID:G53616; PIDN:CAA39439.1; PID:G53617

A:Note: The authors translated the codon AGA for residue 232 as Glu

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide

C:Keywords: cGMP binding; phosphoric diester hydrolase

F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.5%; Score 791; DB 2; Length 856;

Best Local Similarity 27.0%; Pred. No. 1.4e-43;

Matches 228; Conservative 159; Mismatches 325; Indels 134; Gaps 26;

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QY 189 PEEAAGD-QKGAVATNQDKIKQL--CGELVDL-----DASSLQIKVLOYLQOETQ 237
DB 29 PENVAGACDGLADCGSLRELQVBEAALFELVQDMQESVNMERVVFKILRLCTILH 88
QY 238 ASRCCLLLVSDN--LQLSCKVIG--DKVLEE-----EISFPLTTGRLGOVVDKKS 285
DB 89 ADRCSLFWYRQNGVAELATRLFSVQPGSALEDCLVPPDSEIVFPDLIDIGVGHVATKKM 148
QY 286 IQLKDLTS--EDMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTD 340
DB 149 INVQDVABCPHFSSPADELTDV---TKNLTSTPIWN--GKDVAVIMAVNKLDDGPCFTS 203
QY 341 QDEHVIQCHFYTSTVLSTLAFQEKQKKEC---QALLQVAKNLFTHLDDVSVLLQEL 397
DB 204 EDEDVFTKYLNFATLNLK---IYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFKA 260
QY 398 ITEARNLSNAETCSVFLDDQNELVAKVFDGGVV---EDESY----- 435
DB 261 FYTTRAYLNCERYSVGLLDMTK-EKEFFDVWVPLMGEAQPSGPRTPDGREIVFVKVYDI 319
QY 436 ---EIRI-----PAD-----QGIAGHVATTGQILNPDAVAHPL--FYRGVDDSTGPR 478
DB 320 ILHGKEDIKVIPTPPADHWALASGLPTYVAESGFCINMTAADEMFTQEGPLDSDG 379
QY 479 TRNLCFPIKQENQVIGVAELVNKINGPWSKFPEDLATAFSIYCGISIAHSLLYKKVN 538
DB 380 IKNVLSMPTVKNKEBIVGATFYNRKDGKFPDQDEVLMEISLTQFLGWSVLNTDTYDKMN 439
QY 539 EAQYRSHLANEMMYHMKVSDDEYTKLHD-----GIQPVAAATDSNFA----- 581
DB 440 KLENKQIAQDMVLYHVRCDKDEIQILPTRRERLKEPADCEDELGILLKEELPGPTKF 499
QY 582 ---SFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYPDPYHNW 638
DB 500 DIYRPHPSDLECTELELVKCGIQMYVELGVVRKFQIPQEVLRFLFSVSKGYRRITYHNW 559
QY 639 MHAFSVSHFCYLLYKNLELTYNLEMEITAFIPISCMCHDLHRGTNNNSFQVASKSVLAAL 698
```


Db 752 ERTVLOQQPMPMDENKEDLPKLVQGVDFVCTFYVKEFSRPFKEITPMLSLGQNNRVE 811
Qy 875 WTKVSHKFTIRGLPSNNSLDFLEE 899
Db 812 WKSLADEYDAK-----MKVIEEE 829
RESULT 14
S13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13032; S30763
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha
c'ing of the beta-subunit gene.
A:Reference number: S13030; MUID:91130581; PMID:1847109
A:Accession: S13032
A:Molecule type: DNA
A:Residues: 1-800 <BA>
A:Cross-references: UNIPROT:Q62037; EMBL:X60133
R:Baehr, W.
submitted to the EMBL Data Library, June 1991
A:Reference number: S30762
A:Accession: S30763
A:Molecule type: DNA
A:Residues: 1-559,'R',561-800 <BA2>
A:Cross-references: GB:X87952; EMBL:X60133; NID:g871432; PID:g871433
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: alternative splicing; cGMP binding; cGMP binding; phosphoric diester hydrolase
F:556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NP>
Query Match 15.8%; Score 756; DB 2; Length 800;
Best Local Similarity 27.9%; Pred. No. 2.5e-41;
Matches 216; Conservative 142; Mismatches 301; Indels 114; Gaps 23;
Qy 189 PEEAAGD-OKGGVATNQDRKILQI--CGELYDL-----DASSLQKLVQVLOQETQ 237
Db 29 PENVAGACEDGLADCGSLRELQCVESAAFLVQDMQESVNMERVVFKILRLCTLH 88
Qy 238 ASRCLLAVSDN--LQLSCVKIG--DKVLEE-----BISPLTTTGRGQVVEDKKS 285
Db 89 ADRSLFWYRGNGIAELATRLFSVQPSLLEDCLVPDPSEIVPDLDIGVGHVAQYKGM 148
Qy 286 IQLKDLT-----SEDMQOLQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFTD 340
Db 149 INVQDVASCPHFSSPADELTDVY---TKNILLSTPMN--GKDVAVIMAVNKLDPGCPFTS 203
Qy 341 QDEHVIQCHFYHTSTVLSTLAFQEKQLKCEC---QALLQVAKNLFTHLDDVSVLLQRI 397
Db 204 EDEDVFTKYLNFATLNLK---IYHLSYLHNCETRRGQVLLWSANKVFEELTDIERQFHKA 260
Qy 398 ITEARLSNAETCSVFLDDQNELVAKVPDGGV---EDES Y----- 435
Db 261 FYTVRAYLNCBRYSVGLLDMTK-EKEPFDVNPVLMGEAQPTSGRPTDPGRBIVFKVYDY 319
Qy 436 -----EIRI-----PAD-----QGTAGHVAATGQTLINPDYAHPL--FYRGVDDSTGFR 478
Db 320 ILHGKEDIKVIPTPADHWALASGLPTVVASGGFCINMNASADMFNFQSGPLDDSGV 379
Qy 479 TRNLCFPIKNENQEVIGVSLVKNKINGPWSKFDLATAFYSYCGISIAHSLLYKKVN 538
Db 380 IKNVLSMIVNKGEEIVGATFYNRKDGKFPDDQDEVLMESLTOFLGWSVLNTDTYDKN 439
Qy 539 EAQVRSHLANEMMYHMKVSDDEYTKLHD---GIQVVAIIDSNA----- 581
Db 440 KLENKDIQAQMVHLVHVCDDKDETSILPTDRDLGKEPADCEBELGKILKEELPGTKF 499
Qy 582 ---SFTYTPRSLPEDDTSMALSLMQDMNFNNYKIDCPTTLARFCLMYKKGYRPPYHNW 638
Db 500 DIYEFHPSDLCTELELVKCGIQMYELGVVRKFQIPQEVLRFLFSVSKAYRRTIYHNW 559

Qy 639 MHAESVSHFCVLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAAL 698
Db 560 GHGFNVAAQTMTFLMTGKLSYTTDLFAFAMVTAAGLCHDIDHRTGNNNDYQMSQNPLAKL 619
Qy 699 YSSEGSVMERHFAQAIAIINTHGCNIFDHFSDRYQRMMLDRDIIILATDLAHLRIEFK 758
Db 620 HGS--SILERHLEFGKFLAABESLNIYQNLRQRQHEVHILMDIAIATDLALYFKKRT 677
Qy 759 DLQKMAE-----VGYDRTNKQHSLLCLLMTSCDLSQDTGKWTKTRKIAELIY 807
Db 678 MFQKIVDESKNYEDKKSWEYLSLETRKETVMAAMMTACDLSAITTKPWEVQSKVALLVA 737
Qy 808 KEFESQGDLEK-AMGNRPMEMMDREK-AYIPELOISFWEHIAPIYKLLQLDF 858
Db 738 ABFEWQGDLEKTVLDVQQPPIPMMDRNKAELPKLVQGVDFIDFVCTFYVKEPPLGIF 790
RESULT 15
S06418
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
N:Alternate names: cGMP phosphodiesterase alpha chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S06418; S27007; S00161; A34611; S08516
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zha
T.M.; Bystrov, N.S.; Severtsova, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S06418
A:Accession: S06418
A:Molecule type: mRNA
A:Residues: 1-859 <OV1>
A:Cross-references: UNIPROT:P11541; EMBL:X12756; NID:g616; PIDN:CAA31243.1; PID:g617
A:Accession: S27007
A:Molecule type: protein
A:Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3
645;654-663;663-667;703-712;734-736;751-760;766-771;787-798;811-819 <OV>
A:Note: this paper is a translation of the Russian paper published in Dokl. Akad. Nauk S
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ichenko, K.A.; Zagranichny, V.E.;
FEBS Lett. 223, 169-173, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S00161; MUID:88030033; PMID:2822478
A:Accession: S00161
A:Molecule type: mRNA
A:Residues: 1-859 <OV2>
A:Cross-references: EMBL:M27541; NID:g162826; PIDN:AAA30441.1; PID:g162828
A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 381-Val was also found
R:Pittler, S.J.; Baehr, W.; Waemuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: A34611
A:Molecule type: mRNA
A:Residues: 1-193,'V',195-423,'T',425-674,'F',676-859 <PIT>
A:Cross-references: GB:M26043; NID:g162833; PIDN:AAA30443.1; PID:g162834
C:Comment: This protein is involved in the transduction and amplification of the visual p
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P
C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; reti
F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental
Query Match 15.8%; Score 754.5; DB 1; Length 859;
Best Local Similarity 25.8%; Pred. No. 3.5e-41;
Matches 218; Conservative 148; Mismatches 335; Indels 145; Gaps 25;
Qy 189 PEEAAGDOKGGVATNQDRKILQICGLYDLDDASSLQKLVQVLOQETQASRC----- 241
Db 39 PREAAVD-----FSNYH-----ALNSVEEIEITFDLURDQDNLQAEKCVFNWKK 84
Qy 242 -CLLVSEDNLQLSC-----KVIGDKVLEE-----EISFPLTTGRLGQ 278

Db 85 LCFL--QADRLSFWYRARGIAELATRLFNHVDVLEECVLAPDSEIVFPLDMGVVGH 143
Qy 279 VVEDKKSIOQLDTSED---MQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKLGG 335
Db 144 VALSKIVNPN--TEDEHFCDFVDTLTETQKILASPIWN--GKDVVAIIMAVNKVDG 200
Qy 336 DLETQDQEHVIOHCFHYTSTVLSTLAFQEQKLCBEC---QALLQVAKNLFTHLDDVSV 392
Db 201 PHTENDEEILLKYLNFANLIMK---VFHLSYLHNCETRRGQILLMSGSKVFEELTDIER 257
Qy 393 LLOEIIITEARNLSNAEISVFLDDELVAKVPD-----GGVVEDESRYIRI- 439
Db 258 OFHLYTVRAFLNCDRYSVGLLDNTK- QKEFFDVWVPLMGEAPPVAGPRTPDGREINFY 316
Qy 440 -----PAD-----QGIAGHVATTGQILNIPDAYAHL--FYRGVDD 473
Db 317 KVIDYILHGKEDIKVI PNPPDHVALVSGLPTVAQNGLICNIMNAPSEDFFAFQKEPLD 376
Qy 474 STGFRTRNIIICPIKQENQEVIGVAELVNKINGPWFSGFDEDLATAFSIYCGISIAHSL 533
Db 377 ESGWMIKNVLSMFI VNKKEIIVGATFYNRKDGKPFDEMDETLMESLAQFLGWSVLNPD 436
Qy 534 YKVNQAQVESHLANEMMYHMKVSDDEYTKLHD---CIGPVAIDSNFA----- 581
Db 437 YELNKNLENKDIQDMVKYHVCDNREIQITILKTREYVKGKPEWCEEEELAEILOGELP 496
Qy 582 -----SFTYTPRSIPEDDTSMAILSMQDMNFNNYKIDCPTLARFCLMVKGKGYRDP 633
Db 497 DADKYEINKPHFSDLPLETELVKCGIQMYVELKVVDKPHI POEALVRFMYSLSKGYRRI 556
Qy 634 PYNNMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNSFQVASKS 693
Db 557 TYHNRRHGFNVGQTFSLVTGKRYFTDLEALAMVTAFAFCHDIDHRGTNNLYQMSQN 616
Qy 694 VLAALYSSEGSVMERHHFAQAIALINTHGCNIFDHPFRKDYQRMOLDLMDIILATDLAH 753
Db 617 PLAKJHGS--SILERHHLFEFGTKLLRDESLNIFQNLNRQHEHAHMMMDIAITATDALY 674
Qy 754 LRIFKDLQKMAE-----VGYDRTNKQHSLLCLLMTSCDLSDOTKGWKT 799
Db 675 CKKRTWFKQIVDOSKTYETQEQWTOYMMLDOTRKE---IVMAMMTACDLSAITKPWEVQ 731
Qy 800 RKIAELIYKEFFSQGLEK-AMGNRPMEMMDREKA-YIPELQISFMHIAMPIYKLLQDL 857
Db 732 SKVALLVAAEFWEQGLERTVLQONFIPMDNRKADLPKLVQGFIDFVCTFVYKEFSRF 791
Qy 858 FPKAAELYERVASNRHHTKVSHKP--TIRGLPSNNSLDFLDEEYEVPLDGDARAPING- 914
Db 792 HBEITPMLDGIITNNRKWKALADEYETKMKGLEEKQKQAAANQAAAGSQHGKQPGGGP 851
Qy 915 ----CC 916
Db 852 ASKSCC 857

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:56 ; Search time 131.465 Seconds
(without alignments)
3669.244 Million cell updates/sec

Title: US-10-697-894-43
Perfect score: 4911
Sequence: 1 MGACGHSILCRSQYPAAR.....VFDLGRAPINGCCSLDAB 942

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4728.5	96.3	941	1 CN2A_HUMAN	O00408 homo sapien
2	4711.5	95.9	941	2 Q81W54	Q81W54 homo sapien
3	4657	94.8	921	1 CN2A_BOVIN	P14099 bos taurus
4	4418	90.0	928	1 CN2A_RAT	Q01062 rattus norv
5	4366.5	88.9	916	1 CN2A_MOUSE	Q92284 mus musculu
6	3345	68.1	685	2 Q6ZMR1	Q6ZMR1 homo sapien
7	1659.5	33.8	819	2 Q96076	Q96076 ephydratia f
8	1236	25.2	491	2 Q7Q4A0	Q7Q4A0 anophelies g
9	992	20.2	1544	2 Q8MQW0	Q8MQW0 drosophila
10	986	20.1	934	2 Q9HCR9	Q9HCR9 homo sapien
11	986	20.1	988	2 Q96S76	Q96S76 homo sapien
12	986	20.1	1018	2 Q95TW8	Q95TW8 drosophila
13	986	20.1	1131	2 Q9VFI9	Q9VFI9 drosophila
14	983	20.0	1365	2 Q9VJ79	Q9VJ79 drosophila
15	974	19.8	935	2 Q8YB06	Q8YB06 rattus norv
16	950	19.3	1088	2 Q7QD99	Q7QD99 anophelies g
17	938	18.1	856	2 Q6ZC7	Q6ZC7 caenorhabdi
18	938	19.1	859	1 YN66_CABEL	P30645 caenorhabdi
19	923	18.8	883	2 Q6S9E8	Q6S9E8 rattus norv
20	920.5	18.7	684	2 Q6GZY7	Q6GZY7 homo sapien
21	916.5	18.7	852	2 Q6S9E9	Q6S9E9 rattus norv
22	915.5	18.6	779	2 Q6FHX1	Q6FHX1 homo sapien
23	915	18.6	789	2 Q9ULW9	Q9ULW9 homo sapien
24	914	18.6	794	2 Q9QYJ6	Q9QYJ6 rattus norv
25	913.5	18.6	779	1 CN10_HUMAN	Q9Y233 homo sapien
26	912.5	18.6	788	2 Q9QYJ5	Q9QYJ5 rattus norv
27	908	18.5	796	2 Q6S9E2	Q6S9E2 mus musculu
28	907	18.5	843	2 Q7ZM87	Q7ZM87 brachydanio
29	906.5	18.5	685	2 Q8VID7	Q8VID7 rattus norv
30	906.5	18.5	773	2 Q7TFG1	Q7TFG1 mus musculu
31	906.5	18.5	779	2 Q9WV11	Q9WV11 mus musculu

32	906.5	18.5	790	2 Q8CA95	Q8CA95 mus musculu
33	906.5	18.5	797	2 Q7TFG2	Q7TFG2 mus musculu
34	901	18.3	653	2 Q6S9E6	Q6S9E6 rattus norv
35	901	18.3	714	2 Q6S9E7	Q6S9E7 rattus norv
36	899	18.3	714	2 Q9HCP9	Q9HCP9 homo sapien
37	897	18.3	657	2 Q9NTV4	Q9NTV4 homo sapien
38	845.5	17.2	576	2 Q9HB46	Q9HB46 homo sapien
39	841.5	17.1	581	2 Q8VID8	Q8VID8 rattus norv
40	821.5	16.7	854	1 CNRB_HUMAN	P35913 homo sapien
41	805.5	16.4	865	1 CN5A_CANFA	Q77746 canis fami
42	804.5	16.4	862	1 CNRC_CHICK	P52731 gallus gall
43	804	16.4	875	1 CN5A_HUMAN	Q76074 homo sapien
44	801.5	16.3	853	1 CNRB_BOVIN	P23439 bos taurus
45	799	16.3	856	1 CNRB_CANFA	P33726 canis fami

ALIGNMENTS

RESULT 1
ID CN2A_HUMAN STANDARD; PRT; 941 AA.
AC O00408;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
DE GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).
GN Name=PDE2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).
RC TISSUE=Fetal brain, and Hippocampus;
RX MEDLINE=97354299; PubMed=9210593; DOI=10.1016/S0378-1119(97)00046-2;
RA Rosman G.J., Martins T.J., Sonnenburg W.K., Beavo J.A., Ferguson K.,
RA Loughney K.;
RT "Isolation and characterization of human cDNAs encoding a CGMP-
RT stimulated 3',5'-cyclic nucleotide phosphodiesterase.";
RL Gene 131:89-95(1997).
CC -!- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
CC nucleoside 5'-phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=PDE2A3;
CC IsoId=O00408-1; Sequence=Displayed;
CC Name=PDE2A1;
CC IsoId=O00408-2; Sequence=Not described;
CC Name=PDE2A2;
CC IsoId=O00408-3; Sequence=Not described;
CC TISSUE SPECIFICITY: Expressed in brain and to a lesser extent in
CC heart, placenta, lung, skeletal muscle, kidney and pancreas.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -!- SIMILARITY: Contains 1 GAF domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U67733; AAC51320.1; -;
CC Genew; HGNC:8777; PDE2A.

```
DR MIM; 602658; -.
DR GO; 0004118; F:cgmp-stimulated cyclic-nucleotide phosphodi. . .; TAS.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDease.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDease I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; 1.
KW Alternative splicing; CGMP; Hydrolase; Membrane.
FT DOMAIN 372 550 GAF.
FT DOMAIN 633 891 Catalytic (By similarity).
SQ SEQUENCE 941 AA; 105716 MW; 9797609848JFD64E CRC64;

Query Match 96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 2e-273;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGHSILCSQOYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60
DB 1 MGQACGHSILCSQOYPAARPAERPGQVFLKPDPEPPPPPCADSLQDALLSLGSDIV 60
QY 61 AGLOAVKEALSAVLPKVTETVYTYLLDGESRLVCEPPHPELPQEGKVREAVISRKLGCN 120
DB 61 SGLQAVKEALSAVLPVETVYTYLLDGESQLVCEDPHPELPQEGKVREALISRKLGCN 120
QY 121 GLGPSDLPGKPLARLVAFLAPDQVTLVPLVDKESAGAAVAVILVHCQGLSDNEWSLQAV 180
DB 121 GLGPSDLPGKPLARLVAFLAPDQVTLVPLVDKESAGAAVAVILVHCQGLSDNEWSLQAV 180
QY 181 EKHTLVALKRVALQOORESSVAPENATQNPPEAAGDQKGVAYTDDRKILQLCGELYDL 240
DB 181 EKHTLVALLRRVQLQORPREAPRAVQNPPEGAEDQKGGAAATDRDKILQLCGELYDL 240
QY 241 DASSLQLKVLQVLOQETOASRCCLLVSEDNLQLSCKVIGDKVLEERISFPLTTGRLLQGV 300
DB 241 DASSLQLKVLQVLOQETASRCCLLVSEDNLQLSCKVIGDKVLEEVSFPL-TGCLQGV 299
QY 301 VEDKKSILKDLTSEDMMQOLASMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
DB 300 VEDKKSILKDLTSEDVQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 359
QY 361 DODEHVIOHCFTYSTVLVTSILAQKEQKLKCEQALLOVAKNLFTHLDDVSVLLQHIIT 420
DB 360 DEDEHVIOHCFTYSTVLVTSILAQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQHIIT 419
QY 421 EARLNSNAEICSFLLDQNEILVAKVFDGCVVDESEYEIRIPADQGIAGHVATTGQILNIP 480
DB 420 EARLNSNAEICSFLLDQNEILVAKVFDGCVVDDSEYEIRIPADQGIAGHVATTGQILNIP 479
QY 481 DAYAHLPIYRGVDDSTGFRTRNILLCFPIKNEQVEVIGVAELVNKINGFWFSKFDDELATA 540
DB 480 DAYAHLPIYRGVDDSTGFRTRNILLCFPIKNEQVEVIGVAELVNKINGFWFSKFDDELATA 539
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQTPVAADSN 600
DB 540 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQTPVAADSN 599
QY 601 PASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCFLMWKGYRDPYPYNNWM 660
DB 600 PASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCFLMWKGYRDPYPYNNWM 659
QY 661 HAFVSHPFCYLLYKNLELTNYLEDMEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALY 720
DB 660 HAFVSHPFCYLLYKNLELTNYLEDIEIFALPISCMCHDLDRGTNNNSFQVASKSVLAALY 719
QY 721 SSEGVSVMRHHFAQAIALNTHGNCVIFDHFPRKDYQRMQLMRDIIILATDLAHLRIFKD 780
DB 720 SSEGVSVMRHHFAQAIALNTHGNCVIFDHFPRKDYQRMQLMRDIIILATDLAHLRIFKD 779
QY 781 LQKMAEVGYDRTNKQHHSLLCLLMTSCDLSQTKGWKTKTKIAELIYKFFSQGDLEKA 840

Db 780 LQKMAEVGYDRTNKQHHSLLCLLMTSCDLSQTKGWKTKTKIAELIYKFFSQGDLEKA 839
QY 841 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELIYERVASNRHWTQVS 900
DB 840 MGNRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELIYERVASNRHWTQVS 899
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942
DB 900 HKFTIRGLPSNNSLDFLDEEYVDPDLGTRAPINGCCSLDAE 941

RESULT 2
Q8IW54 PRELIMINARY; PRT; 941 AA.
ID Q8IW54
AC Q8IW54
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 2A, cGMP-stimulated.
GN Name=PDE2A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ueffing T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Stalska U., Smailus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040974; AAH40974.1; -.
DR GO; GO:0004114; F:3'; 5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; F:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDease I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; 1.
SQ SEQUENCE 941 AA; 105648 MW; 93028FC28CB54D6B CRC64;

Query Match 95.9%; Score 4711.5; DB 2; Length 941;
Best Local Similarity 95.6%; Pred. No. 2.1e-272;
Matches 901; Conservative 19; Mismatches 21; Indels 1; Gaps 1;
```

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OY 1 MCQACGHSILCRSQYPAARPAEPRGQVFLKPDDEPPPPQPCADSLQDALLSLGSDIV 60
DB 1 MCQACGHSILCRSQYPAARPAEPRGQVFLKPDDEPPPPQPCADSLQDALLSLGSDIV 60
OY 61 AGLQAVKALSAVLPKVETVTVTYLLDGSRLVCEPPELHPOEGKVRKAVLSRKLGN 120
DB 61 SGLQAVKALSAVLPRVETVTVTYLLDGSRLVCEPPELHPOEGKVRKAVLSRKLGN 120
OY 121 GLGSDLPKPLARLVLAPDPTQVLVPLVDKEAGAAVAVLVHCGQLSDNEEWSLQAV 180
DB 121 GLGSDLPKPLARLVLAPDPTQVLVPLVDKEAGAAVAVLVHCGQLSDNEEWSLQAV 180
OY 181 EKHITVALKVALQOQRESSVAPEATONPPBEAGDKGCVAYTODRKILQICELYDL 240
DB 181 EKHITVALKVALQOQRESSVAPEATONPPBEAGDKGCVAYTODRKILQICELYDL 240
OY 241 DASSILQKVLQVLOQETASRCLLVSEDNLQSKVIGDKVLEESFPLTTGRLGV 300
DB 241 DASSILQKVLQVLOQETASRCLLVSEDNLQSKVIGDKVLEESFPLTTGRLGV 300
OY 301 VEDKKSILQKLTSEDVQQLQMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
DB 301 VEDKKSILQKLTSEDVQQLQMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
OY 361 DODEHIVIOHCFHYTSTVLSTLAFQKQKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
DB 361 DODEHIVIOHCFHYTSTVLSTLAFQKQKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
OY 421 EARNLSNAEICSVFLLDQNELVAKVDPGVGVDESVETIRIPADQGIAGHVAITGQLNIP 480
DB 421 EARNLSNAEICSVFLLDQNELVAKVDPGVGVDESVETIRIPADQGIAGHVAITGQLNIP 480
OY 481 DAYAHLPLFVRGDDSTGFRTRNLCFPKIKENQEVIGVAELVKNKINGPWFSDLDATA 540
DB 481 DAYAHLPLFVRGDDSTGFRTRNLCFPKIKENQEVIGVAELVKNKINGPWFSDLDATA 540
OY 541 PSYICGISTAHSLLYKKVNEAQRSHLANEMMYMKVSDDBYTKLLHDGIQPVAAIDSN 600
DB 541 PSYICGISTAHSLLYKKVNEAQRSHLANEMMYMKVSDDBYTKLLHDGIQPVAAIDSN 600
OY 601 FASFTYTPRSIPEDDTSNAILSMLODMFNNYKIDCPTLARFCLVKKGVDPYHNWM 660
DB 601 FASFTYTPRSIPEDDTSNAILSMLODMFNNYKIDCPTLARFCLVKKGVDPYHNWM 660
OY 661 HAFVSFHCYLLYKNLELTNYLEDIEIPALFISCMCHLDHRTGNNNSFOVASKSVLAALY 720
DB 661 HAFVSFHCYLLYKNLELTNYLEDIEIPALFISCMCHLDHRTGNNNSFOVASKSVLAALY 720
OY 721 SSEGSMERHHPAQAIALNTHGCCNI FDHFSKDYORMLDLMDRIILATDLAHLRIFKD 780
DB 721 SSEGSMERHHPAQAIALNTHGCCNI FDHFSKDYORMLDLMDRIILATDLAHLRIFKD 780
OY 781 LQMAEVGYDRNKKOHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGLSKA 840
DB 781 LQMAEVGYDRNKKOHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEPFSQGLSKA 840
OY 841 MGNRMEMMDREKAVIPELOISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
DB 841 MGNRMEMMDREKAVIPELOISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
OY 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAFINGCCSLDAE 942
DB 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAFINGCCSLDAE 942
```

RESULT 3

```
ID CN2A BOVIN STANDARD; PRT; 921 AA.
AC P14099; 028064;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
```

```
DE GMP stimulated phosphodiesterase) (CGS-PDE) (cGSPDE).
GN Name=PDE2A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A1).
RX MEDLINE=91373395; PubMed=1654333;
RA Sonnenburg W.K., Mullaney P.J., Beavo J.A.;
RT "Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide
RT phosphodiesterase cDNA. Identification and distribution of isoyme
RT variants.";
RL J. Biol. Chem. 266:17655-17661(1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM PDE2A3).
RX TISSUE=Brain;
RA Julifs D.M., Sonnenburg W.K., Seraji S., Beavo J.A.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 592-921 FROM N.A.
RX TISSUE=Heart;
RA le Trong H., Beier N., Sonnenburg W.K., Stroop S.D., Walsh K.A.,
RA Beavo J.A., Charbonneau H.;
RT "Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide
RT phosphodiesterase from bovine heart.";
RL Biochemistry 29:10280-10288(1990).
RN [4]
RP SEQUENCE OF 613-694 AND 808-868.
RX TISSUE=Heart;
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;
RT "Identification of a conserved domain among cyclic nucleotide
RT phosphodiesterases from diverse species.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312(1986).
CC -1- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
CC nucleoside 5'-phosphate.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=PDE2A1;
CC IsoId=P14099-1; Sequence=Displayed;
CC Name=PDE2A2;
CC IsoId=P14099-3; Sequence=Not described;
CC Name=PDE2A3;
CC IsoId=P14099-2; Sequence=VSP 004555;
CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -1- SIMILARITY: Contains 1 GAF domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M73512; AAA74559.1; -.
CC EMBL; L49503; AAA87353.1; -.
CC PIR; A40981; A40981.
CC InterPro; IPR003018; GAF.
CC InterPro; IPR003607; Met_phos_hydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF01590; GAF; 2.
CC Pfam; PF00233; PDEase_1; 1.
CC PRINTS; PR00387; PDIESTERASE1.
CC SMART; SM00065; GAF; 2.
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DR	SMART: SMO0471; Hdc: 1.	
DR	PROSITE; PS00126; PREASE I; 1.	
KW	Acetylation; Alternative splicing; cGMP; Direct protein sequencing;	
KW	Hydrolase; Membrane.	
FT	DOMAIN 352 530	GAF.
FT	DOMAIN 613 871	N-acetylmethionine.
FT	MOD RES 1 1	MRRQPAASRDLPAGEPPPGSGDGA -> MQQACGHSILCR
FT	VARSPPLIC 1 25	SOQYPAARPAEPGQVFLKPEDPPPPPPQCADS (in isoform PDE2A3).
FT		/FTid=VSP_004555.
FT	CONFLICT 204 204	N -> D (in Ref. 2).
FT	CONFLICT 633 633	P -> L (in Ref. 4).
SQL	SEQUENCE 921 AA; 103227 MW; 529F4C987583640 CRC64;	
Query Match 94.8%; Score 4657; DB 1; Length 921;		
Best Local Similarity 98.9%; Pred. No. 3.6e-269;		
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;		
Qy	35 EPPPPQPCADSLQDALLSGSVTDVAGLQAAVKEALSAVLPKVTETVYTYLLDGSRLVC 94	
Dy	14 QEPVPPSGDGLQDALLSGSVTDVAGLQAAVKEALSAVLPKVTETVYTYLLDGSRLVC 73	
Qy	95 EEPPELPOEGKREAVTSRRKLCNGLPGSDLPGLRLAVLAPDPTQVLVPLVDKE 154	
Dy	74 EEPPELPOEGKREAVTSRRKLCNGLPGSDLPGLRLAVLAPDPTQVLVPLVDKE 133	
Qy	155 AGAAVAVILVRCGLSDNEEWSLQAVEKHTLVALKRQALQORESSVAPEATQNPPEAA 214	
Dy	134 AGAAVAVILVHCGLSDNEEWSLQAVEKHTLVALKRQALQORESSVAPEATQNPPEAA 193	
Qy	215 GDQGGVAYTQDRKILQCGELVDLASSLQVLQVLOQETOASRCCLLLVSEDNLQ 274	
Dy	194 GDQGGVAYTQDRKILQCGELVDLASSLQVLQVLOQETOASRCCLLLVSEDNLQ 253	
Qy	275 SKVIGDKVLEELSPFLTTGRGQGVEDKKSIOQLKDTSDMQOQSLMCEVQAMLCV 334	
Dy	254 SKVIGDKVLEELSPFLTTGRGQGVEDKKSIOQLKDTSDMQOQSLMCEVQAMLCV 313	
Qy	335 PVISRATDQVVALACAFNKLGGDLTQDQEHVQHCFHYTSTVLSTLAFQEKQKCEC 394	
Dy	314 PVISRATDQVVALACAFNKLGGDLTQDQEHVQHCFHYTSTVLSTLAFQEKQKCEC 373	
Qy	395 QALLQVAKNLFTHLDDVSVLQELITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE 454	
Dy	374 QALLQVAKNLFTHLDDVSVLQELITEARNLSNAEICSVFLLDQNELVAKVFDGGVVEDE 433	
Qy	455 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRTRNLCFPPIKNEQE 514	
Dy	434 SYEIRIPADQGIAGHVATTGQILNIPDAYAHPFLYRGVDDSTGFRTRNLCFPPIKNEQE 493	
Qy	515 VIGVAELVNKINGPWFSEFDELATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMWY 574	
Dy	494 VIGVAELVNKINGPWFSEFDELATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMWY 553	
Qy	575 HKVUSDDBYTKLHDGIQPVAAIDSNFASFTYTPSLPDDTSMALLSMLQDMFNINNYK 634	
Dy	554 HKVUSDDBYTKLHDGIQPVAAIDSNFASFTYTPSLPDDTSMALLSMLQDMFNINNYK 613	
Qy	635 IDCPTLARFCLMWKGYRDPVPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSC 694	
Dy	614 IDCPTLARFCLMWKGYRDPVPHNMHAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSC 673	
Qy	695 MCHDLDRGTNNSFQVASKVLAALYSSEGSVMERHHPAQAIATLTHGNCNIFDHFSRKD 754	
Dy	674 MCHDLDRGTNNSFQVASKVLAALYSSEGSVMERHHPAQAIATLTHGNCNIFDHFSRKD 733	
Qy	755 YQRLMDLMDRIILATDLAHLIRIPKDLQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDT 814	
Dy	734 YQRLMDLMDRIILATDLAHLIRIPKDLQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDT 793	
Qy	815 KGWKTTRKIAELIYKPEFSQGDLEKAMGNRMWMDREKAVIPELQISFMEHIAMPIYKL 874	

Db	794 KGWKTTRKIAELIYKPEFSQGDLEKAMGNRMWMDREKAVIPELQISFMEHIAMPIYKL 853	
Qy	875 LQDLFPKAAELYERVASNRHHTWKVSHKFTIRGLPSNNSLDPLDEEVEVPDLDGARAPIN 934	
Dy	854 LQDLFPKAAELYERVASNRHHTWKVSHKFTIRGLPSNNSLDPLDEEVEVPDLDGARAPIN 913	
Qy	935 GCCSLDAE 942	
Dy	914 GCCSLDAE 921	
RESULT 4		
CN2A_RAT STANDARD; PRT; 928 AA.		
ID	CN2A_RAT	
AC	Q01062;	
DT	01-APR-1993 (Rel. 25, Created)	
DT	01-OCT-1996 (Rel. 34, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic	
DE	GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).	
GN	Name=Pde2a;	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCBI_TaxID=10116;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;	
RX	MEDLINE=95110334; PubMed=7811274;	
RA	Yang Q., Paskind M., Bolger G., Thompson W.J., Repaske D.R.,	
RA	Cutler L.S., Epstein P.M.;	
RT	"A novel cyclic GMP stimulated phosphodiesterase from rat brain.";	
RL	Biochem. Biophys. Res. Commun. 205:1850-1858(1994).	
RN	[2]	
RP	SEQUENCE OF 643-759 FROM N.A.	
RX	MEDLINE=92406782; PubMed=1326532;	
RA	Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;	
RT	"A polymerase chain reaction strategy to identify and clone cyclic	
RT	nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA	
RL	encoding the 63-kDa calmodulin-dependent phosphodiesterase.";	
RL	J. Biol. Chem. 267:18683-18688(1992).	
CC	-1- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP).	
CC	-1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =	
CC	nucleoside 5'-phosphate.	
CC	-1- SUBUNIT: Homodimer (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Membrane-Bound (Potential).	
CC	-1- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=3;	
CC	Comment=Additional isoforms seem to exist. Experimental	
CC	confirmation may be lacking for some isoforms;	
CC	Name=PDE2A3;	
CC	Isoid=Q01062-1; Sequence=Displayed;	
CC	Name=PDE2A1;	
CC	Isoid=Q01062-2; Sequence=Not described;	
CC	Name=PDE2A2;	
CC	Isoid=Q01062-3; Sequence=Not described;	
CC	-1- TISSUE SPECIFICITY: Brain.	
CC	-1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase	
CC	family.	
CC	-1- SIMILARITY: Contains 1 GAF domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; U21101; AAA63683.1; -.	
DR	EMBL; M94540; AAA40922.1; -.	
DR	PIR; JC2486; JC2486.	
DR	RGD; 620965; Pde2a.	

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DR InterPro; IPR003018; GAP.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAP; 2.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAP; 3.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE I; 1.
KW Alternative splicing; cGMP; Hydrolyase; Membrane.
FT DOMAIN 360 538
FT CATALYTIC (By similarity).
FT CATALYTIC 621 879
FT CONFLICT 646 646 W -> R (in Ref. 2).
FT CONFLICT 758 758 L -> M (in Ref. 2).
SQ SEQUENCE 928 AA; 104663 MW; EF0B8C1E266EAB18 CRC64;

Query Match 90.0%; Score 4418; DB 1; Length 928;
Best Local Similarity 92.4%; Pred. No. 6.e-255;
Matches 846; Conservative 31; Mismatches 33; Indels 6; Gaps 2;

QY 25 RQQVFLKPPDEPPPPQPCADSLQDALLSLGSLVIDVAGLQQAVKALSAVLKPVETVITY 84
DB 18 RQQVFLKPPDE--PPQPCCADSLQDALLSLGSLVIDIAGLRQAAXDALSAVLKPVETVITY 75
QY 85 LLDGESRLVCEPPHPELPOEGKVRKAVISRKGLGNGLGPDLPGKPLARLVLAPLDTQ 144
DB 76 LVDGESRLVCEPPHPELPOEGKVRKAVISRKGLGNGLGPDLPGKPLARLVLAPLDTQ 135
QY 145 VLVITPLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPE 204
DB 136 VLVITPLVKEAGAAVAVILVHCGQLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPE 191
QY 205 ATQNPPEBAAGQKGGVAYTDDRKILQLCGELYDLDSLSQLKVLQVLOQBTQASRCLL 264
DB 192 AVQNTSADPSEQDKDEKGTAAHDKILQLCGELYDLDSLSQLKVLQVLOQBTQATHCCL 251
QY 265 LLVSDNQLSKVIGDKVLEBEISFPLTTGRLQGVQVDEKKSILQKLTSDMQQLQSM 324
DB 252 LLVSDNQLSKVIGDKVLEBEISFPLTTGRLQGVQVDEKKSILQKLTSDMQQLQSM 311
QY 325 GCEVQAMLCVPVISRATQVVALACAFNKGDLFTDQDEHVIORCHFTVSTVLTSLAF 384
DB 312 GCEVQAMLCVPVISRATQVVALACAFNKGDLFTDQDEHVIORCHFTVSTVLTSLAF 371
QY 385 QKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLLDQNELVAK 444
DB 372 QKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLLDQNELVAK 431
QY 445 VFDGVDVDESYEIRIPADQGIAGHVATTGQILNIPDAYAHLPLFYRGVDDSDTGFRNII 504
DB 432 VFDGVDVDESYEIRIPADQGIAGHVATTGQILNIPDAYAHLPLFYRGVDDSDTGFRNII 491
QY 505 CFPPIKNEQVIGVAVELNKGMPKSPFDEDLATAFSIYCGISTAHSLLYKKVNEAOYR 564
DB 492 CFPPIKNEQVIGVAVELNKGMPKSPFDEDLATAFSIYCGISTAHSLLYKKVNEAOYR 551
QY 565 SHLANEMMYHMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALLSML 624
DB 552 SHLANEMMYHMKVSDDEYTKLLHDGIQVAAIDSNFASFTYTPRSLPEDDTSMALLSML 611
QY 625 QDMNFINNYKIDCPTLAFCLMVKGYRDPYPHNMHAFSVSHFCYLLYKNLELTYNLED 684
DB 612 QDMNFINNYKIDCPTLAFCLMVKGYRDPYPHNMHAFSVSHFCYLLYKNLELTYNLED 671
QY 685 MEIPALFTSCHCHDLDRGTNSFOVASKSVLAALYSSEGSMERHHFAQAIATLTHGC 744
DB 672 MEIPALFTSCHCHDLDRGTNSFOVASKSVLAALYSSEGSMERHHFAQAIATLTHGC 731
QY 745 NIFDHFSSKDYQRMLDLDRDIILATDLAHLRIFKDLQMAEVGYDRNKKHSHLLCLL 804
DB 732 NIFDHFSSKDYQRMLDLDRDIILATDLAHLRIFKDLQMAEVGYDRNKKHSHLLCLL 791
QY 805 MTSCLSDSQTKGKTRKIAELIYKEFFSQGDEKAMGNRPMEMDMREKAYIPELQISFM 864
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DB 792 MTSCLSDSQTKGKTRKIAELIYKEFFSQGDEKAMGNRPMEMDMREKAYIPELQISFM 851
QY 865 EHIAMPIYKLLQDLFPKAAELIYERVASNREHWTKVSHKFTIRGLPSNNSLDLFDEYEV 924
DB 852 EHIAMPIYKLLQDLFPKAAELIYERVASNREHWTKVSHKFTIRGLPSNNSLDLFDEYEV 911
QY 925 DLDGARAPINGCCSLD 940
DB 912 DLDVTRAPVNGCCSLE 927

RESULT 5
CN2A_MOUSE STANDARD; PRT; 916 AA.
ID CN2A_MOUSE
AC Q92254; O8K2UL;
DT 28-FEB-2003 (Rel. 41, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE cGMP-dependent 3',5'-cyclic phosphodiesterase (EC 3.1.4.17) (Cyclic
DE GMP stimulated phosphodiesterase) (CGS-PDE) (CGSPDE).
GN Name=Pde2a;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP X-RAY CRYSTALLOGRAPHY (2.86 ANGSTROMS) OF 183-549 IN COMPLEX WITH GMP,
RP AND DIMERIZATION.
RX PubMed=12271124; DOI=10.1073/pnas.192374899;
RA Martinez S.E., Wu A.Y., Glavas N.A., Tang X.-B., Turley S.,
RA Hol W.G.J., Beavo J.A.;
RT "The two GAP domains in phosphodiesterase 2A have distinct roles in
RT dimerization and in cGMP binding."
RL Proc. Natl. Acad. Sci. U.S.A. 99:13260-13265 (2002).
CC -1- FUNCTION: Hydrolyzes both cyclic AMP (cAMP) and cyclic GMP (cGMP)
CC (By similarity).
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
CC nucleoside 5'-phosphate.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -1- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC family.
CC -1- SIMILARITY: Contains 1 GAP domain.
CC -----
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DR	ENBL; BC006845; AAH06845.1; -;	
DR	ENBL; BC029810; AAH29810.1; -;	
DR	ENBL; BC057029; -; NOT_ANNOTATED_CDS.	
DR	PDB; IMCO; X-ray; -;	
DR	MGD; MGI:2446107; Pde2a.	
DR	InterPro; IPR002073; PDEase.	
DR	Pfam; PF00233; PDEase_I; 1.	
DR	PRINTS; PR00387; PDIESTERASE1.	
DR	PROSITE; PS00126; PDEASE_I; 1.	
KW	3D-structure; CGMP; Hydrolase; Membrane.	
FT	DOMAIN 348 526	GAF.
FT	DOMAIN 609 867	Catalytic (By similarity).
FT	SITE 421 422	GMP binding.
FT	BINDING 407 407	GMP.
SO	SEQUENCE 916 AA; 103287 MW; 51C03B086633BF20 CRC64;	

Db	709	QAIATLNTGCIIPDFHSRKYQMLDLMRDIIATDLAHLRIIFDQLQKAAEVGIDRNN	768
Qy	794	KQHSLLLLCLLMTSCDLSQDTQGWKTKTKIAELIYKEFFSQGDLEKANGRPMEHMDREK	853
Db	769	QQRHRLLLCLLMTSCDLSQDTQGWKTKTKIAELIYKEFFSQGDLEKANGRPMEHMDREK	828
Qy	854	AYIPELQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHHWTKVSHKFTIRGLPSNNS	913
Db	829	AYIPELQISFMEHTAMPIYKLLQDLFPKAAELYERVASNRHHWTKVSHKFTIRGLPSNNS	888
Qy	914	LDLFDLDEVEYVDDLGGARAPINGCCSLD 940	
Db	889	LDLFDLDEVEYVDDLGGTRAPVNGCCSLE 915	

RESULT 6

Q6ZMR1

ID

Q6ZMR1

PRELIMINARY;

PRT;

685 AA.

AC

Q6ZMR1;

DT

05-JUL-2004

(TrEMBLrel. 27, Created)

DT

05-JUL-2004

(TrEMBLrel. 27, Last sequence update)

DT

05-JUL-2004

(TrEMBLrel. 27, Last annotation update)

DE

Hypothetical protein FLJ16750.

OS

Homo sapiens (Human)

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX

NCBI_Taxid=9606;

RN

[1]

RP

SEQUENCE FROM N.A.

RC

TISSUE=Adrenal gland;

RA

Wanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,

RA

Takebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,

RA

Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Iehli S.,

RA

Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

RA

Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,

RA

Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,

RA

Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,

RA

Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

RL

Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR

EMBL; AK131525; BAD18664.1;

DR

GO; GO:0004114; P:3.5.5-cvcllc-nucleotide phosphodiesterase a.1.1.1; IEA.

Db 102 ----- 101
Qy 265 LLVSEDNLQSKVIGDKVLEEISPLTTGRLGVQVEDKXIQKDLTSEDMDQQLSML 324
Db 102 ----- 101
Qy 325 GCEVQMLCVPVSRATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLSTLAF 384
Db 102 -----FTDEDEHVIOHCFHYTSTVLSTLAF 127
Qy 385 QKEQKLKCEQALLOVAKNLFTHLDDVSVLQEIITEARNLSNAEICSFVLLDQNELVAK 444
Db 128 QKEQKLKCEQALLOVAKNLFTHLDDVSVLQEIITEARNLSNAEICSFVLLDQNELVAK 187
Qy 445 VPDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNL 504
Db 188 VPDGGVDDSEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNL 247
Qy 505 CPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYICGISTAHSLLYKKVNEAQYR 564
Db 248 CPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYICGISTAHSLLYKKVNEAQYR 307
Qy 565 SHLANEMMYHMKVSDDEYTKLHDGIQPVAALDSNFASFTVTPRSLPEDDTSMAILSML 624
Db 308 SHLANEMMYHMKVSDDEYTKLHDGIQPVAALDSNFASFTVTPRSLPEDDTSMAILSML 367
Qy 625 QDMNFNNYKIDCPTLARFCMLVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYLSD 684
Db 368 QDMNFNNYKIDCPTLARFCMLVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYLSD 427
Qy 685 MEIPALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIATLTHGC 744
Db 428 IEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIATLTHGC 487
Qy 745 NIFDHSRKYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLL 804
Db 488 NIFDHSRKYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLL 547
Qy 805 MTSCLSDQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISPM 864
Db 548 MTSCLSDQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISPM 607
Qy 865 EHIANPIYKLDLPFKAELYERVASNREHVTKSHKFTIRGLSPNSNSLDFLDBEYVVP 924
Db 608 EHIANPIYKLDLPFKAELYERVASNREHVTKSHKFTIRGLSPNSNSLDFLDBEYVVP 667
Qy 925 DLDGARAPINGCCSLDAE 942
Db 668 DLDGTAPINGCCSLDAE 685

RESULT 7
096076

ID 096076 PRELIMINARY; PRT; 819 AA.
AC 096076;
DT 01-MAY-1999 (TremBLrel. 10, Created)
DT 01-MAY-1999 (TremBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE EFPDE2
OS Ephydatia fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haploeclerida; Spongiillidae; Ephydatia.
OX NCBI TaxId=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99015760; PubMed=9801141; DOI=10.1016/S0014-5793(98)01150-8;
RA Koyanagi M., Suga H., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
RA Miyata T.;
RT "Ancient gene duplication and domain shuffling in the animal cyclic
RT nucleotide phosphodiesterase family.";
RL FEBS Lett. 436:323-328(1998).
DR EMBL; AB017022; BAA34308.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.

DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_phos_hydro.
DR InterPro; IPR002073; pDease.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; pDease_1; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; pDEASE_1; 1.
SQ SEQUENCE 819 AA; 92145 MW; F4CA1EB8B23A950E CRC64;
Query Match 33.8%; Score 1659.5; DB 2; Length 819;
Best Local Similarity 40.3%; Pred. No. 2.2e-90;
Matches 351; Conservative 160; Mismatches 265; Indels 95; Gaps 11;
Qy 41 QPCADSL---QDALLSLGSDVIDVAGLQQAQKALSAVLPKVETVYTYLLDGSRLVC--- 94
Db 13 RPSVALSGYEDAILGMAAMSPTFTAAKCLRFTPFSSMAGAVALLDTTENNELAYFE 72
Qy 95 -EPPHELFPQEGKREAVISRKRLGCGNLGPGSDLPKGLARLAPLAPDTQVLVPLVDK 153
Db 73 ENDKVTHLPKMGVWDVQR----- 93
Qy 154 EAGAAVAILVHCGQLSDNEEWSLQAEKHTLVALKRVOALQOORESSVAPEATQNPBEA 213
Db 94 -----TLEENYE-RLRLERTTLVAARKVLAHLNSEH-----EKK 127
Qy 214 AGDQKGVAYTDQDRKILQCGELYDLDASSLQQLVQLQOETQASRCLLVSEDLNQ 273
Db 128 RID-----NMLRVCGELIDLDVVSLSIKLKHIMEVSNNAKCTLFYVEDVTOE 175
Qy 274 LSCKVGIDKVLBEESFPLTTGRLGVQVEDKXIQKDLTSEDMDQ---QLQSMGCEVOA 330
Db 176 LVAYTYNGVPLDKERKPVSSSIYGECTTGLINISNV-PODMRNPRIIDIKGYEPH 234
Qy 331 MLCVPIR---ATDQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTVLSTLAFQKE 387
Db 235 LLCIPVKRGAQGSQSVGLVVCNKNDRPPTKHEDEGLYSLHFCSSMLNNTLVYQRE 294
Qy 388 QKLKCEQALLOVAKNLFTHLDDVSVLQEIITEARNLSNAEICSFVLLD--QNELVAKV 445
Db 295 LALKQNEVLLQVAKNLFTHLDDVSVLQEIITEARNLSNAEICSFVLLDQKRSNLVATV 354
Qy 446 FDGGVDESEYIIRIPADQGIAGHVATTGQILNIPDAYAHPLFYRGVDDSDGFRTRNLC 505
Db 355 FNGDVLKERTLIKV--CGGIAGYVAKGTIVNIIVDAQKHQPPFAEVDKSTGFTKHLIC 412
Qy 506 PPIKNEQEVIGVAELVNKINGPWFSEKDEDLATAFSYICGISTAHSLLYKKVNEAQYRS 565
Db 413 PPIMDNNGVVGVAELCNKINGKPTKYDEELARTFSAYCGISYHSLKYETVMASQGRS 472
Qy 566 HLANEMMYHMKVSDDEYTKLHDGIQPVAALDSNFASFTVTPRSLPEDDTSMAILSMLQ 625
Db 473 SLATELMLYHMKIRPELEERATKTPLPVSPFHEMCKLTTPSPLDIKNSADEIAVNSMN 532
Qy 626 DMNFNNYKIDCPTLARFCMLVKGYRDPYPYHNMHAFSVSHFCVLLYKNLELTYLDEM 685
Db 533 EMDLINKQLHPDILARFVIMVKGYRDPYPYHNMHAFSVHFLVLYCCSKSLCLDDL 592
Qy 686 EIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSVWERHHFAQAIATLTHGCN 745
Db 593 EVLALFVSLCHDIDHRGTNNNAFVCSNSTLACYSSSEGSVWERHHLAQTCLILNSPGCN 652
Qy 746 IFDHSRKYORMLDLMDIILATDLAHLRIFKDLQKMAEVGYDRTNKQHHSLLLCLLM 805
Db 653 IFENLSDYRTTIQIQLIDNLTDDIASHLKKLKHQKQWANDGYERSNEPHEHRLMCSLM 712
Qy 806 TSCDLSQTKGKTKRIKAEIYKEFFSQGLEKAMGNRPMEMDMREKAYIPELQISFME 865
Db 713 TSCDLTASCKTWSNKALSILYIYQEFFSQGLEKALGVTPSEMMDRDRAFIPEQQLQFLD 772

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Qy 866 HIAMPYKLLQDLRPPKAAELRYVASREHW 896
Db 773 NIAGPVQLSLRLLPESAAHYTHLDNRQW 803

RESULT 8
ID Q704A0 PRELIMINARY; PRT; 491 AA.
AC Q704A0;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DE EbiP6713 (Fragment)
GN Name=ebiG6713; ORFName=ENSANGG00000005075;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAS01008964; EAL1229.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 1.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR PROSITE; PS00126; PDEASE_I; 1.
FT NON_TER 1
FT NON_TER 491
SQ SEQUENCE 491 AA; 56349 MW; 5416132C4CE42EF3 CRC64;

Query Match 25.2%; Score 1236; DB 2; Length 491;
Best Local Similarity 50.5%; Pred. No. 1.9e-65;
Matches 250; Conservative 91; Mismatches 138; Indels 16; Gaps 8;

Qy 414 LLQRIIEARNLSNAETCSVLLQON--ELVAKVPDGVGVDESYEIRIPADQGIAGHVA 471
Db 4 LLRGVMTAEKELAAARCSLFLDKHGTGLVSKVPFDG---NEASKETRIESGKGIAGYVA 60

Qy 472 TTGQILNIPDAYHPLFYRGVDDSTGFRTRNLCFFPKIKENQEVIGVAELVNKINGPWFS 531
Db 61 QTGKLLNIRNAYQHPLFYKGVDESTGFKTRNLCFFPCDE-EGVIGVAQLCNKLNHFHD 119

Qy 532 KFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYRMKVSDDBYTKLLHDGI 591
Db 120 KCDEEVATAFSVYCGISIMHALVHKQVQKAEARYKLSOELLLYMKVPDTEVNHAAVAK 179

Qy 592 QPVAADS--NPAFTYTPRSLPDDTSMAL-LSMLQDMNFINNYKIDCPTLAFCLMV 647
Db 180 EPDREQDELXYTFPRFDCPRDVKDHALSVQLAMRMFYDLNFVGSFKIHEYKLARFVLLV 239

Qy 648 KKGVRDPYPYHNMHAFSVSHPCYLLYKNLEL--TNYLEDMEIFALFISCMCHDLDRGTN 705
Db 240 QKGYRDPYPYHNMHAFSAVAHFAYSLMMNLRLIERGIITKMGFSFLAAFCDDLDRGIS 299

Qy 706 NSFQVAKSVLAALYSSEGSVNERHFAQAIAIINTHGCNITPDHFSKDYQRMJDLMRDI 765
Db 300 NSYQTQTSPLARYSSSEGSVNERHLSQAICILNDSKSLDGLSTFEFKECIDYLRLE 359

Qy 766 ILATDLAHLRI FKDLQOM-REVGVDRTNKHSHLLCLMTSCDLSDOTGKWTTRKIA 824
Db 360 ILATDLANHFRILPRLKGLRAEYITEGNSQR---LLSLMTITCCDLNDQIKSWTKVQHVA 416

Qy 825 ELIYKEFFSQDLEKAMGNRMWMDREKAYIPELQISFMEHIAMPIYKLLIQDLFPKAAE 884
Db 9 ELIYKEFFSQDLEKAMGNRMWMDREKAYIPELQISFMEHIAMPIYKLLIQDLFPKAAE 884

Db 107 LVVAFEAEGDLEKQMGRLRPNAMDRKKACIPMLQIEFLTIVIRPTPEILVQIIPETGS 476
Qy 885 LYERVASNREHWTKV 899
Db 477 FLDTIDSNRQWERV 491

RESULT 9
Q8MQW0
ID Q8MQW0 PRELIMINARY; PRT; 1544 AA.
AC Q8MQW0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE SD13056p.
GN Name=Pde1l; Synonym=CG10231;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.G., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY122262; AAM52774.1; -.
DR FlyBase; FBgn0032686; Pde1l.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; P:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Met_Phos_hydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase_I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00065; GAF; 2.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 1544 AA; 171689 MW; F5254E0CCDB3D065 CRC64;

Query Match 20.2%; Score 992; DB 2; Length 1544;
Best Local Similarity 32.0%; Pred. No. 3.7e-50;
Matches 246; Conservative 150; Mismatches 306; Indels 66; Gaps 19;

Qy 225 DQDKIILQCGEL-YDLDASSLQKLVLOYLOQETQASRCCLLV-----SEDNLQLSKV 278
Db 493 DEKELIFELVKDICELEVTLCHKILQNVISILLNADRGSFLVQGRGNGDGLK-KCLV 551

Qy 279 -----IGDKVLEEISPLTTGRLGQVVEDKKSIOQLKOLTSDEM--QOLOSMLG 325
Db 552 SKLFDVCPRTVEENQEQDVRVANGTGIAGHVAESGEVNIIPAYQDERNCIDSITG 611

Qy 326 CEVQAMLQVVISRATQVVALACAFNKLGGDLFTDQDEHVIOHCFHYTSTLTSTLAFQ 385
Db 612 YRTKALLCMPIDKSSGD-VIGVAQVINKMNGECFSEIDEKVFSSVLPQCGIGLRNAQLYE 670

Qy 386 KEQKLKCEQALLOVAKNLFTHLDDVSVLQELITEARNLSNABICSVFLDDQNE--LVA 443
Db 671 KSQLEIKRNQVLLDLARMIFEEQSTIEHMFRLITHMQSLTQCQRVQILLVHEADKGSFS 730

Qy 444 KVFD---GGVVEDS-----YEIRIPADQGIAGHVAATTGQILNIPDAYHPLFYRGVDD 494
Db 731 RVDFEANDISEEATSRTPYESRFPINIGITHVATTGETVNVNPNAYEDDRDASVDE 790

Qy 495 STGFRTRNLCFFPKIKENQEVIGVAELVNKINGPWFKFDLATAFSIYCGISIAHSL 554
Db 791 NSCFKHSILCMAIKSLGQIIIGVILINKFNELDTKNDENFVEAFAPFCGMGIHNTHM 850
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Db 831 AELVTSEFFQGRERLEKLTPSAIFDRNRKDELPRLEWIDSICMPLYQALVKVNVK 890
Qy 882 AAEYERVANSREHWTKVSHKFTIRGLPSNNS 913
Db 891 LKPMLDVSATNRSKWEELHQRLLASTASSSS 922

RESULT 11
Q96S76 PRELIMINARY; PRT; 988 AA.
AC Q96S76;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphodiesterase 11A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11121118;
RX MEDLINE=20570133; PubMed=11121118;
RA Yuasa K., Kanch Y., Okumura K., Omori K.;
RT "Genomic organization of the human phosphodiesterase PDE11A gene;
RT Evolutionary relatedness with other PDEs containing GAF domains.";
RL Eur. J. Biochem. 268:168-178(2001).
DR EMBL; AB048423; BAB62713.1; -.
DR EMBL; AB048402; BAB62713.1; JOINED.
DR EMBL; AB048403; BAB62713.1; JOINED.
DR EMBL; AB048404; BAB62713.1; JOINED.
DR EMBL; AB048405; BAB62713.1; JOINED.
DR EMBL; AB048406; BAB62713.1; JOINED.
DR EMBL; AB048408; BAB62713.1; JOINED.
DR EMBL; AB048409; BAB62713.1; JOINED.
DR EMBL; AB048410; BAB62713.1; JOINED.
DR EMBL; AB048411; BAB62713.1; JOINED.
DR EMBL; AB048412; BAB62713.1; JOINED.
DR EMBL; AB048413; BAB62713.1; JOINED.
DR EMBL; AB048414; BAB62713.1; JOINED.
DR EMBL; AB048415; BAB62713.1; JOINED.
DR EMBL; AB048416; BAB62713.1; JOINED.
DR EMBL; AB048417; BAB62713.1; JOINED.
DR EMBL; AB048418; BAB62713.1; JOINED.
DR EMBL; AB048419; BAB62713.1; JOINED.
DR EMBL; AB048420; BAB62713.1; JOINED.
DR EMBL; AB048421; BAB62713.1; JOINED.
DR EMBL; AB048422; BAB62713.1; JOINED.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR003607; Mec_phos_hydro.
DR Pfam; PF01590; GAF; 2.
DR Pfam; PF00233; PDEase I; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00045; GAF; 2.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 988 AA; 111169 MW; 7F678869353DF7EB CRC64;

Query Match 20.1%; Score 986; DB 2; Length 988;
Best Local Similarity 30.7%; Pred. No. 4.4e-50;
Matches 249; Conservative 160; Mismatches 321; Indels 82; Gaps 19;

Qy 164 VHCQSLDSNEWSLQAVEKHTLVAKRVAQALQRESSVAP-----EATQNPPPE-- 211
Db 185 IHVNRTYD-EQVTSRAQPLSSV---RRALLRKASSLPPTAHLSALLERSVNLQYP 240
Qy 212 BAAGDQKGGVAYTQDRKILQCGEL-YDLASSLQLKVLQYLOQFTQASRCCLLLVSED 270
Db 241 PTADYKCHLKKHNERQPFLELVKDISNDLDTLSYKILIFVCLMVADRCSLFLV--E 298
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulyov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard R.J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupeki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*;"
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celnikier S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence;"
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective;"
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review;"
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AE003659; AAF53675.2;
DR FlyBase: FBgn0032686; Pdel1.
DR GO: GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO: GO:0003824; P:catalytic activity; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR003607; Met_phos_hydro.
DR InterPro: IPR002073; PDEase.
DR Pfam: PF01590; GAF; 2.
DR Pfam: PF00233; PDEase_1; 1.

DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00065; GAF; 2.
DR PROSITE; PS00471; HGC; 1.
DR PROSITE; PS00126; PDEase I; 1.
SQ SEQUENCE 1365 AA; 151173 MW; B0562EPDF05012E56 CRC64;
Query Match 20.0%; Score 983; DB 2; Length 1365;
Best Local Similarity 31.2%; Pred. No. 1.1e-49;
Matches 247; Conservative 150; Mismatches 307; Indels 88; Gaps 19;
QY 225 DDDRILQLCGEL-YDLASSLQLKVLQVLOQETASRCCLLV-----SEDNQLQSKV 278
DB 290 DEKELIFELVKDICHNELEVRTLCHKILQNVSLNADRGSFLVQGRGNGPGLK-KCLV 348
QY 279 -----IGDKVLEEEISFPITTRLGQVDEKKSQIKLQJLTDSEDM--QQQSLMLG 325
DB 349 SKLFDVCPRSTVEEMEQQDEVRVANGTGIAGHVAESGEPVNPIDAYQDERFNCIDSLTG 408
QY 326 CEVQAMLCVPVLSRATDQVVALACAFNKLGGDLPTDQDEHVHQHCFHYTSTVLTSLAFQ 385
DB 409 YRTKALLCMPKIDSSGD-VIGVAQVINKMNGECFSEIDEKVFSSYLQFCGIGLRNAQLYE 467
QY 386 KEQKLKCECOALLOVAKNLFTHLDVSVLQELIITEARNLSNAEICSVPLLDQNE--LVA 443
DB 468 KSQLEIKRQVLLDLARIMFEQSTIEHMFRLTHMQSLIOCORVOILLVHEADKGSFS 527
QY 444 KVFD---GGVVEDES-----YEIRPADQGIAGHVAITGQILNIPDAYAHPLFVRGVD 494
DB 528 RVFDPEANDLSEEAATSRTPYESRFPINIGITGHVATTGETVNVNAYEDDRDFDASVDE 587
QY 495 STGPTRNLCFPPIKVENQVIGVAVLNKINGPWFSPDEDLATAFSYICGISTAHSL 554
DB 588 NSCFKHSILCWAINKSLGQIIGVQLINKNFELDTKNDFVFEAFALFCGIGLRNHTM 647
QY 555 YKKNVNAQYRSHLANEMMYMKVSDDEVTKL-----LHGD 590
DB 648 YEKALVAMAKQSVTLLEVLSYHASATMDEAHLRKQKQQAQVGLRQAPLSLPRKKLQRR 707
QY 591 IQPVAADISNFASFTYTPRSLPEDDTSMAILSMLQDMNPINNYKIDCPTLARFCLMVKKG 650
DB 708 LRVPSAVHFLRDLDFKFDIHFDDEDDTLKACLRLMFLDQFVERFHDYEVLCRWLLSVKEN 767
QY 651 YRDPYHNMGAFAFSVSHFCYLLYKMLELTNYLDEMEIFALFISCMCHDLDRGTNNSPQV 710
DB 768 YRNVYHNRHAFNAFNAQMMFALTTQWKIFGEIECLALITGCLCHDLDRGTNNSPQI 827
QY 711 ASKSVLAAALYSSEGSVMERHHPAQAIILNTHGCIPOHFSRKYQYRMLDLARDIILATD 770
DB 828 KASSPLAQLYST--STMEHHHPDQCLMILNPGNOILANLSSDDYCYRIVRVLDEAILSTD 885
QY 771 LAHLRLIFKD---LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTQKGMWTKTKRIABL 826
DB 886 LAVY---FKKGGPFLESVQTSYVVAEPRALLRAMSMTVCDLSAITKPIEKRVADL 942
QY 827 IYKEFFSQGDLEKANGN-RPMEMMDREKA-YIPELQISFMEHIAPIYKLLQDLFPKAAE 884
DB 943 VSSEFFEQDMKQELNITPIDINNREKEDELPMQVNFIDSICLPIVEAFATLSDKLEP 1002
QY 885 LYERVASNREHW-----TKVS-----HKFTIRGLPSNNSL-----DFLDEYEYVP 924
DB 1003 LVQGVDRNRGHVIDLADVTKTKSQDQPEBEQOQNVISNGDCKAMSDDDVAASEAEVA 1062
QY 925 -DLQGARAPING 935
DB 1063 VDSPEKASVNG 1074
RESULT 15
QVID6
ID QVID6 PRELIMINARY; PRT; 935 AA.
AC QVID6,
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:09:51 ; Search time 32.3607 Seconds
(without alignments)
2800.810 Million cell updates/sec

Title: US-10-697-894-43
Perfect score: 4911
Sequence: 1 MGQACGHSILCSQQYPAAR.....VPLDGLGAPINGCCSLDAE 942

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4657	94.8	921	1 A40981	3',5'-cyclic-nucle
2	4418	90.0	928	1 JC2486	3',5'-cyclic-nucle
3	938	19.1	841	1 S24462	probable 3',5'-cyc
4	938	19.1	918	2 D88544	protein R08D7.6 (i
5	821.5	16.7	854	2 A42828	3',5'-cyclic-GMP p
6	804.5	16.4	862	2 I50186	3',5'-cyclic-GMP p
7	804	16.4	875	1 JX0106	3',5'-cyclic-GMP p
8	801.5	16.3	853	2 A36617	3',5'-cyclic-GMP p
9	801	16.3	856	1 A47451	3',5'-cyclic-GMP p
10	794	16.2	875	1 A48719	3',5'-cyclic-GMP p
11	791	16.1	856	2 S30762	3',5'-cyclic-GMP p
12	788	16.0	855	2 A34810	3',5'-cyclic-GMP p
13	758.5	15.4	858	2 JC4520	3',5'-cyclic-GMP p
14	756	15.4	800	2 S13032	3',5'-cyclic-GMP p
15	753.5	15.3	859	1 S06418	3',5'-cyclic-GMP p
16	739.5	15.1	859	2 S13030	3',5'-cyclic-GMP p
17	726	14.8	859	2 B34611	3',5'-cyclic-GMP p
18	696	14.2	393	2 T25590	adenylate cyclase
19	401.5	8.2	859	2 AC2089	hypothetical prote
20	390.5	8.0	664	2 T24459	hypothetical prote
21	383.5	7.8	712	2 S11626	3',5'-cyclic-nucle
22	382.5	7.8	673	2 I61358	3',5'-cyclic-nucle
23	381.5	7.8	549	2 T16769	hypothetical prote
24	380.5	7.7	584	2 B53109	3',5'-cyclic-nucle
25	380.5	7.7	672	2 I61259	3',5'-cyclic-nucle
26	380.5	7.7	886	2 A54442	3',5'-cyclic-nucle
27	379.5	7.7	536	2 I67945	3',5'-cyclic-nucle
28	379	7.7	562	2 I59143	cAMP phosphodiester
29	379	7.7	564	2 A40949	cyclic-AMP phospho

30	375	7.6	610	2 I67946	3',5'-cyclic-nucle
31	375	7.6	844	2 I53865	phosphodiesterase
32	374	7.6	564	2 JC1519	3',5'-cyclic-nucle
33	374	7.6	736	2 I61354	phosphodiesterase
34	363.5	7.4	777	2 S65543	3',5'-cyclic-nucle
35	350	7.1	519	2 T14783	hypothetical prote
36	345.5	7.0	534	1 A44162	3',5'-cyclic-nucle
37	343.5	7.0	535	1 A46378	3',5'-cyclic-nucle
38	341.5	7.0	535	1 A44161	3',5'-cyclic-nucle
39	341	6.9	530	1 A45334	3',5'-cyclic-nucle
40	340	6.9	768	2 T10796	3',5'-cyclic-nucle
41	335.5	6.8	536	1 JG6129	3',5'-cyclic-nucle
42	330.5	6.7	860	2 A82044	adenylate cyclase
43	329	6.7	267	2 B33904	cAMP phosphodiester
44	327	6.7	498	2 A47286	3',5'-cyclic-AMP p
45	325.5	6.6	323	2 S55348	3',5'-cyclic-nucle

ALIGNMENTS

RESULT 1

A40981
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - bovine
N:Alternate names: cGMP-dependent phosphodiesterase
C:Species: Bos primigenius taurus (cattle)
C:Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C:Accession: A40981; A36112; B26650; A60179; C26650
R:Sonnenburg, W.K.; Mullaney, P.J.; Beavo, J.A.
J. Biol. Chem. 266, 17655-17661, 1991
A:Title: Molecular cloning of a cyclic GMP-stimulated cyclic nucleotide phosphodiesterase
A:Reference number: A40981; MUID:91373395; PMID:1654333
A:Accession: A40981
A:Molecule type: mRNA
A:Residues: 1-921 <SON>
A:Cross-references: UNIPROT:P14099; GB:M73512; NID:9162829; PIDN:AAA74559.1; PID:9162830
R:Lee Ironing, H.; Beier, N.; Sonnenburg, W.K.; Stroop, S.D.; Walsh, K.A.; Beavo, J.A.; Cha
Biochemistry 29, 10280-10288, 1990
A:Title: Amino acid sequence of the cyclic GMP stimulated cyclic nucleotide phosphodiester
A:Reference number: A36112; MUID:91104948; PMID:2176866
A:Accession: B36112
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 592-921 <LET>
A:Accession: A36112
A:Molecule type: protein
A:Residues: 1-203, 'D', 205-477, 'Q', 479-921 <LET2>
R:Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A:Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterases
A:Reference number: A26650; MUID:87092242; PMID:3025833
A:Accession: B26650
A:Molecule type: protein
A:Residues: 613-632, 'L', 634-794; 808-868 <CHA>
A:Experimental source: heart
R:Tanaka, T.; Hockman, S.; Moos Jr., M.; Taira, M.; Meacci, E.; Murashima, S.; Manganieli
Second Messengers Phosphoproteins 13, 87-98, 1991
A:Title: Comparison of putative cGMP-binding regions in bovine brain and cardiac cGMP-st
A:Reference number: A60179; MUID:92065414; PMID:1659635
A:Accession: A60179
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 311-803, 'DV', 806-921 <TAN>
A:Note: part of this sequence was confirmed by protein sequencing
C:Comment: This protein is not glycosylated.
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-
C:Keywords: acetylated amino end; alternative splicing; cAMP binding; cGMP binding; homo
F:635-857/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 94.8%; Score 4657; DB 1; Length 921;
Best Local Similarity 98.9%; Pred. No. 3.4e-293;
Matches 898; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy	35	EPPPPQPCADSLQDALLSLGSDVIDVAGIQQAVKEALSAVLPKVEVTYYTLLDGESRLVC	94
	:	:	:
Db	14	QEPVPPGSGDQALQDALLSLGSDVIDVAGIQQAVKEALSAVLPKVEVTYYTLLDGESRLVC	73
Qy	95	BEPPHELPOBQKVRRAVISRKELGNGLGPSDLPGKPLARLAPADPTQVLVPLVUDKE	154
Db	74	BEPPHELPOBQKVRRAVISRKELGNGLGPSDLPGKPLARLAPADPTQVLVPLVUDKE	133
Qy	155	AGAAVTLVHCQGLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA	214
Db	134	AGAAVTLVHCQGLSDNEEWSLQAVEKHTLVALKRVQALQORESSVAPEATQNPPEEA	193
Qy	215	GDQKGVAYTDQDKIQLCGELYDLDDASSLQKVLQYLQOBTQASRCCLLLVSDNLQL	274
Db	194	GDQKGVAYTDQDKIQLCGELYDLDDASSLQKVLQYLQOBTQASRCCLLLVSDNLQL	253
Qy	275	SKVJGDKVLEBEEISFPITTBRLGQVVEDKKSIOAKDLTSEDMDQLOQSMGCEVQAMLCV	334
Db	254	SKVJGDKVLEBEEISFPITTBRLGQVVEDKKSIOAKDLTSEDMDQLOQSMGCEVQAMLCV	313
Qy	335	PVISATQOVVALACAFNKLGDLPDQDEHVIQCHFYTSTVLTSLTAFQKEQKLKCSC	394
Db	314	PVISATQOVVALACAFNKLGDLPDQDEHVIQCHFYTSTVLTSLTAFQKEQKLKCSC	373
Qy	395	QALLQVAKNLTFLHDDVSVLQEQIITEARNLSNABEICSVFLDDQNELVAKVFDGGVVEB	454
Db	374	QALLQVAKNLTFLHDDVSVLQEQIITEARNLSNABEICSVFLDDQNELVAKVFDGGVVEB	433
Qy	455	SYEIRIPADQGIAGHVATTGQILNPDAVAHPLFYRGVDDSDGFRTRNLCPPIKNENOS	514
Db	434	SYEIRIPADQGIAGHVATTGQILNPDAVAHPLFYRGVDDSDGFRTRNLCPPIKNENOS	493
Qy	515	VIGVABLUNKINGPWFSPDEDLATAPSTYCGISIAHSLLYKKVNEAQYRSHLANEMMY	574
Db	494	VIGVABLUNKINGPWFSPDEDLATAPSTYCGISIAHSLLYKKVNEAQYRSHLANEMMY	553
Qy	575	HMKVSDDBEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMQDMNFPINNYK	634
Db	554	HMKVSDDBEYTKLLHDGIIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSMQDMNFPINNYK	613
Qy	635	IDCPTLARFCLMVKKGYRDPYPYHNMMHAFSVSHFCYLLYKNLELTYLNMEDMEIFALFISC	694
Db	614	IDCPTLARFCLMVKKGYRDPYPYHNMMHAFSVSHFCYLLYKNLELTYLNMEDMEIFALFISC	673
Qy	695	MCHDLDRHGTNNSPQVASKSVLAALYSSEGSVNERHHFAQAIALNTHGCNIFDHFSRKD	754
Db	674	MCHDLDRHGTNNSPQVASKSVLAALYSSEGSVNERHHFAQAIALNTHGCNIFDHFSRKD	733
Qy	755	YQRMLDLMDRDIILATDLAHLRIIFKDLQKMAEYGYDRTNKKQHSLLLCILMTSCDLSQDT	814
Db	734	YQRMLDLMDRDIILATDLAHLRIIFKDLQKMAEYGYDRTNKKQHSLLLCILMTSCDLSQDT	793
Qy	815	KGWKTRTKIAELIYKEFFSQGDEKAMGNRPMMMDREKAYIPELQISPEMHIAMPIYKL	874
Db	794	KGWKTRTKIAELIYKEFFSQGDEKAMGNRPMMMDREKAYIPELQISPEMHIAMPIYKL	853
Qy	875	LQDLFPPKAAELYERVASNREHWTKVSHKFTTIRGLFPSNNSLDFLDBEYEVDPDLDGARAPIN	934
Db	854	LQDLFPPKAAELYERVASNREHWTKVSHKFTTIRGLFPSNNSLDFLDBEYEVDPDLDGARAPIN	913
Qy	935	CCCSLDAAE	942
Db	914	CCCSLDAAE	921

R;Yang, Q.; Paskind, M.; Bolger, G.; Thompson, W.J.; Repaske, D.R.; Cutler, L.S.; Epstein
Biochem. Biophys. Res. Commun. 205, 1850-1858, 1994
A:Title: A novel cyclic GMP stimulated phosphodiesterase from rat brain.
A:Reference number: JC2486; MUID:95110334; PMID:7811274
A:Accession: JC2486
A:Molecule type: mRNA
A:Residues: 1-928 <YAN>
A:Cross-references: UNIPROT:Q01062; GB:U21101; NID:g706933683.1; PID:g70693301
A:Experimental source: brain
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase, cGMP-stimulated; 3',5'-cyclic-
C:Keywords: alternative splicing; cAMP binding; cGMP binding; homodimer; phosphoprotein
F:643-865/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homolog <GNP>
F:109/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match	90.0%;	Score 4418;	DB 1;	Length 928;
Best Local Similarity	92.4%;	Pred. No. 1e-277;		
Matches	846;	Conservative 31;	Mismatches 33;	Indels 6; Gaps 2
Qy	25	RQGVFLKPBEP	PPPCADSLQDALLSLGSDVDVAGLQQAQKVALSAVLPKVETVYTY	84
Db	18	RQGVFLKPB	--PPPPCADSLQDALLSLGAVIDIAGLRQAKDALSAVLPKVETVYTY	75
Qy	85	LLDGSERLVCEB	PHPELPOBQEKVREAVISRKRLGNGCLGSPDLPGKPLARLVAPLAPDTQ	144
Db	76	LVDGESRLVCEB	PHPELPOBQEKIREAVISRKRLSCDGLGPDLLGKPLARLVAPLAPDTQ	135
Qy	145	VLVPLVYDKEAGA	VAAVLVHCGQLSNEEWSLQAVEKHTLVALKRVQALQORESSVAPE	204
Db	136	VLVPLLDLGTGT	VAAVLVHCGQLSDEEQLQVVEKHALVQVRQALQQR----	191
Qy	205	ATQNPPEAAAGD	QKGGVAYTDQDRKILQLCGELYDLDSLQLKVLQYLQEQTOASRCL	264
Db	192	AVQNTSADP	SEDDQKDEGYTAHDKRILQLCGELYDLDSLQLKVLRLYQEQTOATHCL	251
Qy	265	LLVSEDNLQ	LSCKVIGDKVLEEBEISPELTTGRLQGVVEDKKSILQKDLTSEDMQQLSML	324
Db	252	LLVSEDNLQ	LSCKVIGSKVLGEEVSPFLTMGRLGQVVEDKQCIQLKDLTSDVDQQLNML	311
Qy	325	GCEVOAMLCP	VPVISRATDQVVALLACAFNKLGGDLFTDODEHVIQHCPHYTSTVLSTLAF	384
Db	312	GCELRAMLCP	VPVISRATDQVVALLACAFNKLGGDFTDEDERAIQHCPHYTGTVLSTLAF	371
Qy	385	QKEQKLKCEQ	ALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNELVAK	444
Db	372	QKEQKLKCEQ	ALLQVAKNLFTHLDDVSVLQEIITEARNLSNABICSVFLDDQNELVAK	431
Qy	445	VFDGGVVEDSE	YEIRIPADQGIAGHAVTTGQILNIPDAYHPLFYRGVDDSTGTPRTRNL	504
Db	432	VFDGGVVDDE	SEYEIRIPADQGIAGHAVTTGQILNIPDAYHPLFYRGVDDSTGTPRTRNL	491
Qy	505	CFPIKNEQ	EVIGVAELVNKINGPWFSKFDBDLATAFSIYCGISIAHSLLYKYNVEAQVR	564
Db	492	CFPIKNEQ	EVIGVAELVNKINGPWFSKFDBDLATAFSIYCGISIAHSLLYKYNVEAQVR	551
Qy	565	SHLANEMW	MYHKVSDDEYTKLLHDGQPVAAIISDNFASPYTPRSLPDDTSMALLSML	624
Db	552	SHLANEMW	MYHKVSDDEYTKLLHDGQPVAAIISDNFANFYTPRSLPDDTSMALLSML	611
Qy	625	QDMNFNNY	KIDCPTLAFCLMWKGYRDPYPHNMHAFSVSHFCYLLYKNELENTYLED	684
Db	612	QDMNFNNY	KIDCPTLAFCLMWKGYRDPYPHNMHAFSVSHFCYLLYKNELENTYLED	671
Qy	685	MEIPALFIS	CMCHDLDRHTGNTNSFQVASKSVLAALYSEGGVMERHHPAQAIALINTHGC	744
Db	672	IEIPALFIS	CMCHDLDRHTGNTNSFQVASKSVLAALYSEGGVMERHHPAQAIALINTHGC	731
Qy	745	NIPDHF	SRKDYQRMLDLWRDIIILATDLAHLIRIPKDLQKMAEVGVDRTNKHHSLLCLL	804
Db	732	NIPDHF	SRKDYQRMLDLWRDIIILATDLAHLIRIPKDLQKMAEVGVDRTNKHHLCLL	791
Qy	805	MTSCDLS	DQTKGWKTKRIAEFLIYKSFPSQGDLEKAMGNRPMEWMDREKAVIPELQISPM	864
Db	792	MTSCDLS	DQTKGWKTKRIAEFLIYKSFPSQGDLEKAMGNRPMEWMDREKAVIPELQISPM	851

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RESULT 2
JC2486
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cGMP-stimulated - rat
N:Alternate names: cGMP-dependent phosphodiesterase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C:Accession: JC2486

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QY 865 EHIAPIYKLLQDLFPKAAELYERVASNREHWTVKSHKFTIRGLSPNNSLDPLDBEYV 924
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Db 852 EHIAPIYKLLQDLFPKAAELYERVASNREHWTVKSHKFTIRGLSPNNSLDPLDBEYV 911
|||||
QY 925 DLDGARAPINGCCSLD 940
|||||
Db 912 DLDVTRAPVNGCCSLE 927
|||||
RESULT 3
S24452
probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) R08D7.6 - Caenorhabditis
N:Alternate names: hypothetical protein R08D7.6
C:Species: Caenorhabditis elegans
C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C:Accession: S41041; S24462
R:Ainscough, R.; Hawkins, T.
submitted to the EMBL Data Library, May 1992
A:Reference number: S41036
A:Accession: S41041
A:Molecule type: DNA
A:Residues: 1-841 <AIN>
R:Cross-references: UNIPROT:P30645; EMBL:Z12017
R:Sulston, J.; Du, Z.; Thomas, K.; Wilson, R.; Hillier, L.; Staden, R.; Halloran, N.; G
awkins, T.; Ainscough, R.; Waterston, R.
Nature 356, 37-41, 1992
A:Title: The C. elegans genome sequencing project: a beginning.
A:Reference number: S24457; MUID:92168156; PMID:1538779
A:Contents: annotation
C:Genetics:
A:Introns: 31/1; 97/3; 179/2; 260/1; 296/3; 324/3; 622/2; 701/3; 775/3
C:Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase R08D7.6
C:Keywords: phosphoric diester hydrolase
F:403-627/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NCNP>
Query Match 19.1%; Score 938; DB 1; Length 841;
Best Local Similarity 33.1%; Pred. No. 1.4e-52;
Matches 219; Conservative 120; Mismatches 226; Indels 96; Gaps 13;
QY 271 NLQLSCKVIGDK-----VLEEISPLTTGRIGQVVEDKKSIIQLKDLTSDMQQLQSLMLG 325
|||
Db 72 NLQMLKNGRTKDDWGASLRDIETPSGLL-ELLPD----- 108
|||
QY 326 CEVQMLCVPVISRATDQVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTSTLAFQ 385
|||
Db 109 -----VPIVRKLSRPLVKM-----DDQDACSVA NESDRTVLSPLVPM 148
|||
QY 386 KEQKLKCEQALLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQ----- 438
|||
Db 149 IFDQFLC-----LTNNL-----SALISCIIEAKKNTAEADYAVFLHDEDNKQV 194
|||
QY 439 --NE---LVAKVFDGQVDESEYIRIPADQGIAGHVAATTGQILNIPDAYAHLPLFYRGVD 493
|||
Db 195 FNNETMLMTGKKFDWG-----YGIVGKVASWTMTNIRDVSRCPFFNEID 240
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QY 494 DSTGRTENILCFPIKNENQEVIGVAELVNKINGPWFSEKFDLATAFSYIGSIAHSL 553
|||
Db 241 EQFSIKARNLAFPLIDSSCSLIGVILYNKENG--FSRHDEKIKRFSYFVANSIAHAI 298
|||
QY 554 LYKKVNEAQYRSHLANEMMY--HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSL 611
|||
Db 299 LAKQIEEVRTRIHMVVEEFKIQGEDAVIEVDIMRLVNDPLRDWRVFSQNFADSPPPRSV 358
|||
QY 612 PEDDTMAILSMLQDMFINNYKIDCPTLARFCLMKVKGYPDPVPHNWNHAFSVSHFCYL 671
|||
Db 359 GENHFRASMMFFEDLGFSMLYKLNKRLSVLVRVSAGYRVPVPHNWNHAFVATHFCWL 418
|||
QY 672 LYKLELTNYLDEMEIFALFSCMCHDLDRGTNNNSFQVAS--KSVLAALYSSEGSVMER 729
|||
Db 419 TLRTDAIRRALSDMERLSIIACLDIDHRTGTTNSFQMSLQKTPLSVLYSTEGSVLER 478
|||
QY 730 HHFAQAIALNTHGNCIDYHFSRKYQRMLOLMRDIIILATDLAHLRIFKDLQKMAEYGY 789
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Db 479 HHFAQTIKLOOECSILENLPADFRVTIVTREVILATDISAHLRQKERIKTMISEY 538
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QY 790 DRTNKQHSLLLCLIMTSCDLSDOTKGWKTTRKIAELIYKEFFSQDLEKAMGNRPMNM 849
|||
Db 539 NPMSPDHRYLMLCLVMTASDLSQAKNFHNAKRIAENIYLEFFAQGDLEQLGVKPLEMM 598
|||
QY 850 DREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTVKSHKFTIRGLP 909
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Db 599 DRTNAYVPTQIDFLFKIGVFPVQLLASVWPVEGRTTSEIDANHLCHLWALDEE--VRNNP 656
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QY 910 S 910
|||
Db 657 S 657
|||
RESULT 4
D88544
protein R08D7.6 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D88544
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/Projects/C/el
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A:Accession: D88544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-918 <STO>
C:Cross-references: UNIPROT:P30645; GB:chr_III; PIDN:CAA78052.1; PID:g3878939; GSPDB:GNC
C:Genetics:
A:Gene: R08D7.6
A:Map position: 3
C:Superfamily: Caenorhabditis probable 3',5'-cyclic-nucleotide phosphodiesterase R08D7.6
Query Match 19.1%; Score 938; DB 2; Length 918;
Best Local Similarity 33.1%; Pred. No. 1.6e-52;
Matches 219; Conservative 120; Mismatches 226; Indels 96; Gaps 13;
QY 271 NLQLSCKVIGDK-----VLEEISPLTTGRIGQVVEDKKSIIQLKDLTSDMQQLQSLMLG 325
|||
Db 149 NLQMLKNGRTKDDWGASLRDIETPSGLL-ELLPD----- 185
|||
QY 326 CEVQMLCVPVISRATDQVALACAFNKLGGDLFTDQDEHVIQCHFYHTSTVLTSTLAFQ 385
|||
Db 186 -----VPIVRKLSRPLVKM-----DDQDACSVA NESDRTVLSPLVPM 225
|||
QY 386 KEQKLKCEQALLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSVFLDQ----- 438
|||
Db 226 IFDQFLC-----LTNNL-----SALISCIIEAKKNTAEADYAVFLHDEDNKQV 271
|||
QY 439 --NE---LVAKVFDGQVDESEYIRIPADQGIAGHVAATTGQILNIPDAYAHLPLFYRGVD 493
|||
Db 272 FNNETMLMTGKKFDWG-----YGIVGKVASWTMTNIRDVSRCPFFNEID 317
|||
QY 494 DSTGRTENILCFPIKNENQEVIGVAELVNKINGPWFSEKFDLATAFSYIGSIAHSL 553
|||
Db 318 EQFSIKARNLAFPLIDSSCSLIGVILYNKENG--FSRHDEKIKRFSYFVANSIAHAI 375
|||
QY 554 LYKKVNEAQYRSHLANEMMY--HMKVSDDEYTKLLHDGIQPVAAIDSNFASFTYTPRSL 611
|||
Db 376 LAKQIEEVRTRIHMVVEEFKIQGEDAVIEVDIMRLVNDPLRDWRVFSQNFADSPPPRSV 435
|||
QY 612 PEDDTMAILSMLQDMFINNYKIDCPTLARFCLMKVKGYPDPVPHNWNHAFSVSHFCYL 671
|||
Db 436 GENHFRASMMFFEDLGFSMLYKLNKRLSVLVRVSAGYRVPVPHNWNHAFVATHFCWL 495
|||
QY 672 LYKLELTNYLDEMEIFALFSCMCHDLDRGTNNNSFQVAS--KSVLAALYSSEGSVMER 729
|||
Db 496 TLRTDAIRRALSDMERLSIIACLDIDHRTGTTNSFQMSLQKTPLSVLYSTEGSVLER 555
|||

QY 730 HFAQAIAIINTHGCNIFDHSRKYQRMMLDMDIILATDLAHLRIKFDLQMAEVGY 789
Db 556 HFAQITIKLQOECSEILNIPAAADFTIVNTREVILATDISAHLRQERIKTMISEGY 615
QY 790 DRTNKQHSLLCLLMTSCDLSDOTKGWTKTKAELIYKEFFSGDLEKAMGNRMBMM 849
Db 616 NPMSEFDRYLLMCLVNTASDLSQXKNFNKRAENIYLEFFAQQDLEQLGVKPLEMM 675
QY 850 DREKAYIPELOISFMEHIAMPYIKLQDLFPKAAELYERVAENRHHWTKVSHKFTIRGLP 909
Db 676 DRTNAYVPTQIDLEFKIGVDFVOLLASVPEGRITTSIDAIDANHLWCWALDEE--VRNRP 733
QY 910 S 910
Db 734 S 734

RESULT 5
A42828
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - human
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42828; S34590; S18715
R:Collins, C.; Hutchinson, G.; Kowbel, D.; Riess, O.; Weber, B.; Hayden, M.R.
Genomics 13, 698-704, 1992
A:Title: The human beta-subunit of rod photoreceptor cGMP phosphodiesterase: complete re
A:Reference number: A42828; MUID:92347868; PMID:1322354
A:Accession: A42828
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-854 <COL>
A:Cross-references: UNIPROT:P35913; GB:S41458; NID:g252252; PIDN:AAB22690.1; PID:g252253
A:Note: sequence extracted from NCBI backbone (NCBIN:109783, NCBI:P:109784)
R:Khramtsov, N.V.; Feshchenko, E.A.; Suslova, V.A.; Shmukler, B.E.; Terpugov, B.E.; Raki
FEBS Lett. 327, 275-278, 1993
A:Title: The human rod photoreceptor cGMP phosphodiesterase beta-subunit. Structural stu
A:Reference number: S34590; MUID:93351644; PMID:8394243
A:Accession: S34590
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-854 <KHR>
A:Cross-references: EMBL:X66142; NID:g396492; PIDN:CAA46932.1; PID:g396493
R:Weber, B.; Riess, O.; Hutchinson, G.; Collins, C.; Lin, B.; Kowbel, D.; Andrew, S.; So
Nucleic Acids Res. 19, 6263-6268, 1991
A:Title: Genomic organization and complete sequence of the human gene encoding the beta-
A:Reference number: S18715; MUID:92066478; PMID:1720239
A:Accession: S18715
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-314,'Q',316-319,'L',321-359,'R',361-697,'I',699-854 <WEB>
A:Cross-references: EMBL:X62694
C:Genetics:
A:Gene: GDB:PDS6B; PDSE
A:Cross-references: GDB:125915; OMIM:180072
A:Map position: 4p16.3-4p16.3
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.7%; Score 821.5; DB 2; Length 854;
Best Local Similarity 27.5%; Pred. No. 5e-45;
Matches 229; Conservative 158; Mismatches 326; Indels 119; Gaps 25;
QY 209 PPEAAGQKGGVAYTDQDKIQLCGELYD-LDASSLQLKVLQVLOQETQASRCCLLLV 267
Db 41 PPD---CDSLDLQVEBETALLELVQDMQESINWVVKVLRRLCTLLQADRCSLFMY 97
QY 268 SEDN--LQLSCVKVIG---DKVLEE-----EISFPLTGRLGQVVEDKXSIQLKMDT-- 313
Db 98 RQRNGVAELATRLFSVQPDVLEDCLVPPDSEIVFPDIDIGVVGHVQAQTKMNVNVEDAEC 157
QY 314 ---SEDMQQLQSLGCEVQMLCVPIVSRATDQVVALACAFNKLGGDLFTDQDEHVQHC 370

Db 158 PHFSFADELTDY---KTKMNLATPIMN--GKQVVAVIMAVNKLNGPFSTSEDEDFLKY 212
QY 371 FHYTSTVLSTLAFQKQKCEC---QALLQVAKNEFTHLDDVSVLLQELIITEARNLSN 427
Db 213 LNPATLYLK---IVHLSYLHNCETRRGQVLWSANKVFEELTDIERQHKAFYTVRAYLN 269
QY 428 AETCSVELLDQNELVAKVFGGVV---EDSEY-----EIR 459
Db 270 CERYSGVLLDMTK-EKEFFDVMSVLMGESQYSGRPTPDGRIEIVFYKVIDYLHGKEIK 328
QY 460 I---PAD---OGIAGHVATTGQILNI PDAYAHPL--FYRGVDDSTGFRTRNLCFPI 508
Db 329 VIPTPSADHWALASGLPSYVAESGFCINIMNASADEMKFOEGALDUSGLIKVLSNPI 388
QY 509 KNENQEVIGVAELVNKINGPMFSKDEDLATAPSIYCGISIAHSLLYKKNVNEAQVRSHLA 568
Db 389 VNKKEIVGVATFYNRKDGKPFDEQDEVLMESLTQFLGWSVMNTDTYDKMKNLENKRDIA 448
QY 569 NEMMYMKVSDDEYTKLLHD----GIQPVNAIDSNFA-----SFTYTP 608
Db 449 QDMVLYHVKCDRDEIQILPTRARLKGEPADCDDEDELGEILKEBLPGPTTFDIYEFHFS 508
QY 609 RSLPEDDTSMALSMLODMNFINNYKIDCPTLARFCLMKVKGYPDPYVHNMWHAFSVGHF 668
Db 509 LECTELDLVKCGIQNYELGVKRFQIPQEVLVLPFLPSISKGYRITYHNRHGFVNAQT 568
QY 669 CYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALYSSEGSYME 728
Db 569 MFTLLMTGKLKSYTDLFAFAMVTAGLCHDIDHRTGNNLYQMKSQNPLAKLHGS--SILE 626
QY 729 RHHPAQAIATLNTGHCNIFDHSRKYQRMMLDMDIILATDLAHLRIKFDLQMAE-- 786
Db 627 RHHLFEQKFLSEETLIYQNLNRQHEVHILMDIAIATDLALYFKKRAMFOKIVDES 686
QY 787 -----VGYDRTNKQHSLLLCLLMTSCDLSDOTKGWTKTKAELIYKEFFSQDGL 837
Db 687 KNYQDKSWEYLSLETRKEIVNMMWMTACDLSAITKFWQSVQKVALVAEFWEQDGL 746
QY 838 EK-AMGNRPMEMMDREK-AVYPELOISFMEHIAMPYIKLQDLFPKAAELYERVAENRHH 895
Db 747 ERTVLDQOPIPMMDRNKAAELPKLVGFIDFVCTFYVKEFSRPFHEELPMDRLQNNRKE 806
QY 896 WTKVSHKFTIRGLSPNSNLSDFLDEYVDP-----LDGARAPING--CCSL 939
Db 807 WKALADEYEAK----VKALEEKEEERVAACKVGTETCNGGPAPKPSSTCCIL 854

RESULT 6
150186
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50186
R:Sample-Rowland, S.L.; Green, D.A.
Exp. Eye Res. 59, 365-372, 1994
A:Title: Molecular characterization of the alpha'-subunit of cone photoreceptor cGMP pho
A:Reference number: I50186; MUID:95121406; PMID:7821382
A:Accession: I50186
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-862 <SEM>
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C:Keywords: cGMP binding; phosphoric diester hydrolase
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 16.4%; Score 804.5; DB 2; Length 862;
Best Local Similarity 27.7%; Pred. No. 6.4e-44;
Matches 220; Conservative 137; Mismatches 302; Indels 135; Gaps 24;
QY 215 GDQKGGVAYTDQDKIQLCGELYD-----DASSLQL---KVLQVLOQETQASRCCLL 265

Db 42 GGVKGVSPKMSR--LEECNLFELLTBIOBAGSMKIVHKTLQRLSOLLARDRCSMF 99
Qy 266 LVS-----EDNLQSKVIGDKVLEEEISFPPLTTGRLGQVVEDK 304
Db : : : : :
100 ICRSRGPEVATRLNVTPTSKFEDNL-----VNPDK-----ETVPFLDIGIAGVAHTK 150
Qy 305 KSIQKDLTSED--MOQLOSMGCEVOAMLCVPVISRATDQVVALACAFNKLGGDLFTDQ 362
Db : : : : :
151 KFPNPDVKNNHPSDYLDDKTYTNNMAIPITQ--GKEYLVAVMALNKLNASFEFSKB 208
Qy 363 DEHVLQHCFTYSTVL---TSTLAFQKEQKLCCEQALQVAKNLFTHLDDVSVLQRI 418
Db : : : : :
209 DEEVFKYILFISLVLRNHTSYL--YNIESR---RSQMLLSANKVFEELTDIERQFKA 264
Qy 419 ITEARNLSNAEICSVPFLDQNLVAKVFDGGVV---EDES-----456
Db : : : : :
265 LYTIRMVLCNRYSGVGLDWTK--EKEFYDEWPRLGEAEPYKPKTPDQREVNFYKIIDY 323
Qy 457 -----ETRI-----OGIAGHVATTGQILNTPDAYA--HPLFYRGVDDSTGPR 499
Db : : : : :
324 ILHGKEEIKVPTPPADHWHCLISGLPTYVAENGFCINMMNAPADBYFTFQKGPVDETGW 383
Qy 500 TNNILCFPTKNENQEVIGVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLYKKN 559
Db : : : : :
384 IKNVLSLPVNVKKEBIVGATPYNRKDGKPFDEYDEQIITLTQFLGWSVLNNTDTYDKN 443
Qy 560 EAQYRSHLANEMMYHMKVSDDEYTKLLHD---GIQPVAAIDS-----599
Db : : : : :
444 KLENKDTAQEMLMYQTKATPTVESILKYKEKLVNKSIEECDEKDLIRLKEELDPKD 503
Qy 600 -NFASFTYTPRSLPDDTSMALSMQDNFNINNYKIDCPTLARFCLMVYKGYRPPYHN 658
Db : : : : :
504 LELYEFPSPDPVTEHGLITCGIRLPFEINNVYKFKVPAEVLTRWNYTVKGYRDIYHN 563
Qy 659 WMAHSAVSHFCVLLYKNLENTYLEDMEIFALFISCMCHDLHRCNTNNSFQVASKVLAA 718
Db : : : : :
564 WRHGFNVQGTMTLLMTGRKKYKYYTDLEAFAMVAAAFCHIDHRCNTNLYQMKSAAPLAK 623
Qy 719 LYSSEGSVNERHHAQAATLNTGNCNIPDFSRKDYQRMLDLRRDIIATDLAHLHRTF 778
Db : : : : :
624 LHGS--SILERHHLBYSKTLLODESINIFONLKNQEPETVHLFVAVIATDLALYFKKR 681
Qy 779 KDLQKMAE-----VGYDRTNKHSHLLCLLMTSCDLSDOTGKWTTRKIA 824
Db : : : : :
682 TMFQKIVDAIEKMETEEAAIKVISIDPTKCE--VIMAMMTGCDLSAITTKPWEVQSKVA 738
Qy 825 ELIYKEFFSQGLEK--AMGNRRPMEMMDREKA--YIPELQISFMEHTAMPYKLLQDLFPKA 882
Db : : : : :
739 LMVANEFWEQGLERTVLQOQPIPMWDRNKGDELPLKQVGFIDFVCTFYVYKEFSRPHKEI 798
Qy 883 AELYERVASNREHW 896
Db : : : : :
799 TPFMDGLQNNRVEW 812

RESULT 7

JW0106
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - human
N:Alternate names: PDE5A1
C:Species: Homo sapiens (man)
C>Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C:Accession: JW0106
R:Stacey, P.; Rulten, S.; Dapling, A.; Phillips, S.C.
Biochem. Biophys. Res. Commun. 247, 249-254, 1998
A>Title: Molecular cloning and expression of human cGMP-binding cGMP-specific phosphodi-
A:Reference number: JW0106; MUID:98308101; PMID:9642111
A:Accession: JW0106
A:Molecule type: mRNA
A:Residues: 1-875 <STA>
A:Cross-references: UNIPROT:O76074; GB:AJ004865; NID:G3355605; PIDN:CAA06170.1; PID:G335
C:Genetics:
A:Gene: GDB:PDE5A
A:Cross-references: GDB:9032947

C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodi-
C:Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydrolase
F:612-835/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:102/Binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predicted

Query Match 16.4%; Score 804; DB 1; Length 875;

Best Local Similarity 28.7%; Pred. No. 7e-44; Mismatches 322; Indels 124; Gaps 29;
Matches 242; Conservative 154;

Qy 125 SDLPCKPKLARLVA-----PLAPDPTQVLVPLVDKEAGAAVAVILVHCGOLSDNEEWSLOA 179

Db : : : : :
91 NSVPTPTPKISASFFDRLP-----LVKDKSE-GTVSP-----LSDSE-----129

Qy 180 VEKHTLVALKRVQALQORESSVAPATQNPPEAAGDQGGVAYTDDQRKILQLCGELYD 239

Db : : : : :
130 -----KKEQMLTPPPRFDHDEG-----DQCSRLLELVKDISS 161

Qy 240 -LDASSLQLVLOYLQOETQASRCCLLLVSDN-----LQLSKCVIGDKVLEEE---1 288

Db : : : : :
162 HLDVTALCHKIPLTHGLISADRYSLFLVCESSNDKFLISRLFDVABEGSTLSEVSNCCI 221

Qy 289 SPPLTTGRLGQVVEDKKSQKLDLTSEDNQ---QLQSMGCEVOAMLCVPVISRATDQV 345

Db : : : : :
222 RLEWNGKIVGHVAALGEPENIKD--AYEDPRFNAEVDQITGYKTQSILCMP--IKNHRREV 279

Qy 346 ALACAFNKLGGD--LFTDQDEHVIQHCFTYTSVTLTSTLAFQKEQKLCCEQALQVAKN 403

Db : : : : :
280 GVAQAINKSGNGGTFTEKDEKDFAYLAFCGIVLHNAQLYETSLLENKRNQVLLDLASL 339

Qy 404 LPTHLDVSVLQELIITEARNLSNAEICSVELLDQN-----ELVAKVPDGGV 450

Db : : : : :
340 IFEEQOSLEVLNKKIAATIIISFMQVQKCTIFIVDEDCDSFSFVHMECEELEKSDTUT 399

Qy 451 VEDESYETRIPADQGIAGHVATTGQILNIPDAYAHPFVYRGVDDSTGFR---TRNLCFP 507

Db : : : : :
400 REHDANKI-----NYMYAQVYVNTMEPLNIPDVSKDRPFWTENTGNVNNQOCIRSLCTP 455

Qy 508 IKN-ENQEVIGVAELVNKINGPW-----FSKPEDEDLATAFSIYCGISIAHSLYKKNB 561

Db : : : : :
456 IKNGKKNKIVGVQCLVNKMEENTGKVKPFNRNDEQFLEAFVIFCGLGIQNTQMYEAVERA 515

Qy 562 QYRSHLANEMMYHMKVSDDEYTKL--LHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMA 619

Db : : : : :
516 MAKQMTLEVLVSYHASAAABEETRELQSLAAAVVP--SAOTLKITDFSFDFELSDLETALC 574

Qy 620 ILSLQMDNFNINNYKIDCPTLARFCLMVKKGVR--DPPYNNMMAHAFSVSHFVLLYKQLBL 678

Db : : : : :
575 TIRMTDNLVQNFQMKHEVLCRWLSVKKNYKRVAVYNNWHAFTAQCMFAALKAGKI 634

Qy 679 TNYLEDMEIFALFISCMCHDLHRCNTNNSFQVASKVLAAALYSSEGSVNERHHAQAIAI 738

Db : : : : :
635 QNKLTDLSEILALLIAALSHDLHRCVNNYSIQRSEHPLAQLYCH--SIMEHHHFDQCLMI 692

Qy 739 LNTGNCNIPDFSRKDYQRMLDLRRDIIATDLAHLR-----IFKDLQKMAEYGVDRTNK 794

Db : : : : :
693 LNSPGNQILSGLSIEEYKTLKIIKQAILATDLALYIKRGEFFELIRKNQ---FNLEDP 749

Qy 795 QHHSLLCLLMTSCDLSDOTGKWTTRKIAELIYKEFFSQGLE--KAMGNRRPMEMMDREK 853

Db : : : : :
750 HQKELFLANLMTACDLSAITKPWPIQRIAEVLATEFPDQGRERKELNIEFTDLANREK 809

Qy 854 A-YIPELQISFMEHTAMPYKLL-----QDLFPKAAELYERVASNREHMTKVS---HKFTI 905

Db : : : : :
810 KNIKPSMQVGFDAICLQLYEALTHVSEDCFP-----LLDGGCKRNQKQKQALAAEQEOKMLI 865

Qy 906 RG 907

Db 866 NG 867

RESULT 8

A36617
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta chain - bovine

N/Alternate names: cGMP phosphodiesterase beta chain
C/Species: Bos primigenius taurus (cattle)
C/Date: 28-Mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004
C/Acession: A36617; S19145; S14011; S00251
R/Lipkin, V.M.; Khrantsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.; Muradov, K.G.; Gub J. Biol. Chem. 265, 12955-12959, 1990
A>Title: Beta-subunit of bovine rod photoreceptor cGMP phosphodiesterase. Comparison with A/Reference number: A36617; MUID:90330632; PMID:2165490
A/Acession: A36617
A/Molecule type: mRNA
A/Residues: 1-853 <LIP>
A/Cross-references: UNIPROT:P23439; GB:J05553; NID:g162824; PIDN:AAA30440.1; PID:g162825
A/Experimental source: retina
A/Note: 40-Arg was also found
R/Lipkin, V.
submitted to the EMBL Data Library, December 1990
A/Reference number: S19145
A/Acession: S19145
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-853 <LI3>
A/Cross-references: EMBL:X57146; NID:g209; PIDN:CAA40436.1; PID:g210
R/Lipkin, V.M.; Gubanov, V.V.; Khrantsov, N.V.; Vasilevskaya, I.A.; Atabekova, N.V.; Mu Bioorg. Khim. 16, 118-120, 1990
A>Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the bet A/Reference number: S14011; MUID:90267525; PMID:2161230
A/Acession: S14011
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2,'P', 4-90,'P', 92-93,'H', 95-202,'VN', 205-489,491-853 <LI2>
R/Ovchinnikov, Y.A.; Gubanov, V.V.; Khrantsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.; FEBS Lett. 223, 169-173, 1987
A>Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp A/Reference number: S00161; MUID:88030033; PMID:2822478
A/Acession: S00251
A>Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 534-536,'RRSNC',542-596,'Y',598-601,'W',603-606,'QLI' <OV>
C/Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide P Keywords: acetylated amino end; blocked amino end; cGMP; cGMP binding; phosphoric di F/2-853/Product: 3',5'-cyclic-GMP phosphodiesterase beta chain #status predicted <MAT> F/556-789/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F/2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 16.3%; Score 801.5; DB 2; Length 853;
Best Local Similarity 26.2%; Pred. No. 9.8e-44;
Matches 221; Conservative 169; Mismatches 333; Indels 119; Gaps 23;

Qy 201 VAEATONPPEEAAGDOKGVAY-----TDQRKILQLCGELYD-LDASLSQIKVLYIQ 254
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
27 LSPEDVANACED--GCPEGCTSFRELQCVEESAALFELVDQMDENVNMERVPFKILLRLC 84
Qy 255 QETOASRCCLLVSEDN--LQLCKTVIG---DKVLBE-----EISFPLLTTLGLQOWVE 302
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
85 SILHADRCSLFMTRQMGVAELATRLFPSVPDSVLEDCLPDPSEIVFPDLIDVGWHVAQ 144
Qy 303 DKRSIQLKOLT-----SEDNQQLQSMGLGCEVQAMLCVPVISRATQDVVALACAFNLGGD 357
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
145 TKGMVNVQDMVECPHFSSPADELTDVV---TRNILATPIMN--GKDVAVIMAVMVKLDGP 199
Qy 358 LFTDDHEVTHQCFHYHTSTVLTSLFAQEKCLKCEC---QAIIQVAKNFLTHLDDVSVL 414
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
200 CFTSSEDDVF---LKYLNFGTLNKLKYHLNYLHCNCTRGRQVLLWSANKVFESLTDIRQ 256
Qy 415 LQEITTEARNLSNAEICSVFLDQNE-----LVAKV 445
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
257 FHKAFTYRAYINCDSRVSGLLDMTKKEFFDWPVLMGEAQAYSGRPDPDGREILFYKV 316
Qy 446 PDGWWEDESYEIRI-----PAD-----QGIAGHVATTGQILNTIPDAYAHPL---FYRGVDD 494
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
317 ID---YLHGKEDIKVIPTPPADHWALASGLPTVAESGFCINWNAPADMENFQSGPLD 374

Db	29	PEHVACGCGQPTDCASRELQVBSAALFELVQDMQESVNMVERVVPFKILRLCTILR	88
Qy	259	ASRCCLLLVSDN--LQLSCKVIG---DKVLEB-----EISFPATTGRLGQVVEDKXS	306
Db	89	ADRCSLFMYQRNGVAELATRLPSVQGSAGDECLVPPDSEIVFPFLDIGVGVHVAQTKM	148
Qy	307	IQLKDLTS--EDMQLOQLMGCEVQAMLCVPVTSRATDQVVALACAFNKLGGDLPTDQD	364
Db	149	VNVQDVTECFHPSFPFADELGTGYETRNILATPINV--GKEVAVVIMALKNDGCPCTSEDE	206
Qy	365	HVIQCHFYHTSVTLTSTLAFQEKQKCEC---QALLQVAKNLFTHLDVSVLLOBIITE	421
Db	207	DVTF---LKLNFCTLNKLYHLSYLNCHETRRGQVLLNSANKVFEELTIERQFHKAFTY	263
Qy	422	ARNLSNAEICSVPLLDQNELVAKVPDGGVV---EDBSY-----	456
Db	264	VRAYLNCDRYSVGLLDMTK-EKEFFDVPVLMGEAQYSGPRTPDGRREIVFYKVIDYLH	322
Qy	457	---EIRI---PAD-----QGIAGHVATTGOILNIPDAYAHL--PYRGVDDSTGPRTRN	502
Db	323	GKEDIKVIPSPADHWALASGLPTYVAESGFCINIMNTAADDEMFTFQEGFLDDSGWVIKN	382
Qy	503	ILCFPTKNGNOEIVGVAELVKNKINGPWFSKFDEDLATAFSYCGISIAHSLLYKKVNEAQ	562
Db	383	VLSMPIVNKKEELVGATFTYNRKDGKPFDEQDEVLMESLQFLGWSVLNIDTYDKNKKDE	442
Qy	563	YRSHLANEMMYHMKVSDDEYTKLHD---GIQPVAAIDSNFA-----	602
Db	443	NRKDIADQNVLYHVRCDKDEIQLLPTRELKGPADCEDELGILLKEVLPGPSKFDIY	502
Qy	603	STYTPRSLPEDDTSMAILSMLODMNFINNYKIDCPTLARPCLMVKKGVRDPPYNNHMA	662
Db	503	EFHFSLECTELELVKCGIQMYELGVGRKFQIPQEVLRFLFSVSKGYRRITYHNWRHG	562
Qy	663	FSVSHFCYLLYKNLETLNLEMEIPALFISCMCHDLDRGTNNNSFOVASKSVLAALYS	722
Db	563	FNAQTMFTLLTGGKLSYTTDLFAFMYTAGLCHDIDHRGTNNLYOMKSQNPALKLHGS	622
Qy	723	EGSVMERHHFAQAIATLNGCNIQDFHSRKYQYRMLDLMRDIILATDLAHLRIFKDIQ	782
Db	623	--SILERHLEFGKFLSETLNIYQNLNRQHEVHLMDIAITATDLALFYKKTWTFQ	680
Qy	783	KMAE-----VGYDRTNKHHSLLCLLMTSCDLSQDTGKWKTKTKIAELIYKBF	831
Db	681	KIVDESKNYEDRKSWVEYLSLETTREKIVVAMMTACDLSAITKEWQSVKALLVAAEF	740
Qy	832	FSQGLEK-AMGNRPMMMDREK-AVPELOISPMEHIAPIYKLLQDLFPKAAELYERV	889
Db	741	WEOGLERTVLDQOPIPMMDRNKAALPKLQVGFIDFVCTFYKGFERSFHEBILPMFDR	800
Qy	890	ASNREHWTKVSHKFTIRGLPSNNSLDLDEEYVDP-----LDGARAPING-C	936
Db	801	QNNRKEWALADEYAK-----LKALBEEKQQQEDRTAKAGTEICNGGPAPKSTC	853
Qy	937	CSL 939	
Db	854	CIL 856	

RESULT 10

A48719
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) 5A - bovine
N/Alternate names: PDE5A1
C/Species: Bos primigenius taurus (cattle)
C/Date: 26-Aug-1999 #sequence_revision 26-Aug-1999 #text_change 26-Aug-1999
C/Accession: A48719; A35807
R/McAllister-Lucas, L.M.; Sonnenburg, W.K.; Kadlecsek, A.; Seger, D.; Le Trong, H.; Colbran, R.J. Biol. Chem. 268, 22863-22873, 1993
A/Title: The structure of a bovine lung cGMP-binding, cGMP-specific phosphodiesterase de
A/Reference number: A48719; M01D:94043054; PMID:8226796
A/Accession: A48719
A/Molecule type: mRNA
A/Residues: 1-875 <MCA>

A/Cross-references: GB:I16545			
A/Experimental source: lung			
R/Thomas, M.K.; Francis, S.H.; Corbin, J.D.			
J. Biol. Chem. 265, 14971-14978, 1990			
A/Title: Substrate- and kinase-directed regulation of phosphorylation of a cGMP-binding			
A/Reference number: A35807; MUID:90368672; PMID:2168396			
A/Accession: A35807			
A/Molecule type: protein			
A/Residues: 90-101 <THO>			
C/Superfamily: 3',5'-cyclic-GMP phosphodiesterase 5A; 3',5'-cyclic-nucleotide phosphodi-			
C/Keywords: alternative splicing; cGMP binding; phosphoprotein; phosphoric diester hydr			
F:602-825/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>			
F:92/binding site: phosphate (Ser) (covalent) (by cGMP-dependent kinase) #status predic			
Query Match 16.2%; Score 794; DB 1; Length 875;			
Best Local Similarity 28.4%; Pred. No. 3.1e-43;			
Matches 240; Conservative 154; Mismatch 334; Indels 116; Gaps 29;			
Qy	125	SDLPKPKLARLVA-----PLAPDTQVLVPLVDKAGAAVAAVILVHCGGLSDNEEWSLQA	179
Db	81	SSVPGTPTRKISASBFRPLRP-----IVIKDSE-GTVSF-----LSDSD-----	119
Qy	180	VEKHTLVALKRYOALQORESSVAPATQNPPEAAAGDKGVAYTDQDRKILQLCGELYD	239
Db	120	-----KKEQMLTSPRFDNEG-----DQCRLELVLKDIS	151
Qy	240	LDASSLQIKVLQYLOQETQASRCCLLLVSDN-----LQLSCKVIGDKVLEEE---I	288
Db	152	HLDTALCHKIPLHIGHLISADRYSLFLVCEDSSNDKFLISLFDVAEGSTLEASNCCI	211
Qy	289	SPFLTTRGLQGVREDKKSIQLKDLTSEDNQ---QLQSMGCEVQAMLCVPVTSRATDQV	345
Db	212	RLWNKGIHVHVAAGEPLNKKD-AVEDPRFAEVDQITGYKTQSILCMP-INKHREYV	269
Qy	346	ALACAFNKLGD--LFTDQDEHVIQCHYHTSVTLTSTLAFQEKQKLCCECQALQVAKN	403
Db	270	GVAQAINKKSGNGTFTKDEKDFAAFLAFQGVILHNAQLYETSLLENKRNQVLLDLASL	329
Qy	404	LFTLDDVSVLQETITEARNLSNAEICSVFLDQ--NELVAKVPDGGVVEDESVEIRP	461
Db	330	IFEEQOSLEVLKKTAAITIIISPMQVKCTIFIVDEDCSDSPSSVFHMECEELEKSDTLT	389
Qy	462	ADQG-----IAGHVATTGOILNTPDA---YAHPLFYRGVDDSTGFRTRNLLCPPIKN-	510
Db	390	RERDANRINYMYAQVYKVTMEPLNIPDVSKDKRFPFTNMENMGNIQQCIRSLCTPIKNG	449
Qy	511	ENQEVIGVAELVNKINGPW-----PSKEDEDLATAFSYCGISIAHSLLYKKVNEAQYRS	565
Db	450	KKNKIVIGCOLVNKMEETTGKVFAPNRNDEQLEAFVIFCGLGIQNTQMYEAVERAWAKQ	509
Qy	566	HLANEMMYHMKVSDEYTKL--LHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMAILSM	623
Db	510	MYTELVSYHASAAEETRELQSLAAAVVP-SAQTLLKTDTSFSDSFELSDLETALCTIRM	568
Qy	624	LQDMNFINNYKIDCPTLARPCLMVKGYR-DPPYNNHMHAFSVSHFCYLLYKNLELTNYL	682
Db	569	FTDLNLVQNFQMKHEVLCWKILLSVKKNYKKNVAYHNWRHAFNTAQCMFAALKAGKIQKRL	628
Qy	683	EDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALYSSEGSVMERHHFAQAIILNTH	742
Db	629	TDLEITALLIALSHDLDRGVNNSYIQRSEHPLAQLYCH--SIMEHHHFDQCLMLNSP	686
Qy	743	GCNIFDHFSDKYQRMMLDMRDIILATDLAHLR---IFKDQKMAEVGVYDRTNKQHS	798
Db	687	GNQILSGUSTEIKYTKLIIQAILATDLALYIKRGEFFELIMKNQ---FNLEDPHQKE	743
Qy	799	LLCLLMTSCDLSQDTGKWKTKTKIAELIYKEFFSQGDLE-KAMGNRPMMMDREKA-YI	856
Db	744	LFLAMLATCDLSAITKWPICQRIAEVLVATEFFDQGRERKELNIEPADLNREKKNKI	803
Qy	857	PELQISPMEHIAPIYKLL---QDLFPKAAELYERVASNRHWTKVS---HKFTIRGLP	909
Db	804	PSMQVGFTDAICLQLYEALTHVSEDCFP-----LLDGCRRKRNQKQALAEQOEKTLINGS	859

Db 60 LLEVLLE-EGAGVELAAHRAALQRLAQLQADRCMSFLCRARNGTPEVASKLLDVTPTSKF 118
QY 269 EDNLQLSCRVIGDKVLEEEISFPLTTGRLGQGVVEDKKSQQLKDL--TSBDMQOOLSMGLGC 326
Db 119 EDNL-----VVPDR-----BAVFPDLVGIVGVAHTKTKFTNPDVKNSHSPDMDKQGY 169
QY 327 EQVAMLCVPVISRATDOVVALLACAFNKLGGDLFTDQDEHVIQHCFTYTSVLV---STLA 383
Db 170 VTRNLATPIV--MGKEVLAVFMAVNVKVDASEFSDQDEVFYSKLSFVSIILKLHHTNYL 227
QY 384 FQKEOKLKCECQALLQVAKNLFTHLDDVSLQLEIITEARNLSNAEICSVELLDQNELVA 443
Db 228 YNIESR---RSQILMWSANKVFEELTVERQPHKALYTVTRTYLNCERYSIGLDMWK-BK 283
QY 444 KVFDDGW---BDESY-----EIRI-----PAD-----QGI 466
Db 284 EFDWEPVKGVEPYKPKTPDREVIKYKIIDVILHGKEIKVPTPPMDHWTLLISGL 343
QY 467 AGHVATTGQILNIPDAYA--HPLFYRGVDDSTGPRTRNLCPPIKNEQEVIGVABLNVK 524
Db 344 PTYVAENGFCNMLNAPADEYTFQKGPVDETGWIKNVLSPVNVKKEDIVGVATFYNR 403
QY 525 INGPFSKPEDLATAFSYCGISIAHSLLYKKNVQVRSHLANEMMMYHMKVSDDEYT 584
Db 404 KDGKPFDEYDEHIAETLTQFLGWSLNTDTYKMKNKLENKRKDIAQEMLMNHTKATPDEIK 463
QY 585 KLLH-----DGIQVAAIDSNFAS-----FTYTPRSIP--EDDTSMAILSM 623
Db 464 SILKFKERKNIDVIEDCEBKQLVILKEDLPDPRADLYEPFRHLPITEHELIKGLURL 523
QY 624 LQDMFNNYKIDCPTLAFCLMVKGYRDPDPHYHNMHAFSVSHFCYLLYKNLELTNYLE 683
Db 524 FPEINNVKFKPVEVLTWMTYTRKGYRAVTVYHNRHGFNVGTWFTILLMTGLRKKYTT 583
QY 684 DMEIFALFISCMCHDLDRGTNNNSFOVASKVLAALYSEGSVMRHHFAQAIATLNTHG 743
Db 584 DLFAFAMLAAPACHDIDHRGTNNLYQMKSTSPLARLHGS--SILERRHLEYSKTLLODES 641
QY 744 CNIPDHSRKYQRMLDLMDRIILATDLAHLIRIFKDLQKMAE-----VGY 789
Db 642 LNIFQNLNKRQVETVHLFEVAILIATDLALYFKKRTMKQIVDACEKMETEBEAIKYITI 701
QY 790 DRNTKQHSLLLCLLMTSCDLSQDKGWKTKTKIAELIYKEFPFSGDLEK-AMGNRPMEM 848
Db 702 DPTKKE---IIMAMMTACDLSAITKPEVQSQVALLVANEFWEQGLERTVLQQQPIPM 758
QY 849 MDR-EKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTYVSHKP 903
Db 759 MDRNKKDELPLKQGVFIDPVCTFYVYKFSFRHKEITPMLNGLQNNRNVKSLADBY 814

RESULT 13
JC4520
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha' chain - human
C:Species: Homo sapiens (man)
C>Date: 08-Feb-1996 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: S63688; JC4520
R:Feishchenko, E.A.; Andreava, S.G.; Suslova, V.A.; Smirnova, E.V.; Zagranichny, V.E.; Li
FEBS Lett. 381, 149-152, 1996
A>Title: Human cone-specific cGMP phosphodiesterase alpha' subunit: complete cDNA sequen
A:Reference number: S63688; MUID:96193933; PMID:8641425
A:Accession: S63688
A:Molecule type: mRNA
A:Residues: 1-858 <FES>
A:Cross-references: UNIPROT:P51160; EMBL:X94354; NID:g1616594; PIDN:CAA64079.1; PID:g114
A>Note: Intron positions were determined by partial sequencing of genomic DNA
R:Vicizian, A.S.; Piriev, N.I.; Farber, D.B.
Gene 166, 205-211, 1995
A>Title: Isolation and characterization of a cDNA encoding the alpha' subunit of human c
A:Reference number: JC4520; MUID:96125191; PMID:8543163
A:Accession: JC4520
A:Molecule type: mRNA

A:Residues: 1-115, 'V', 117-269, 'S', 271-372, 'P', 374-463, 'L', 465-564, 'Q', 566-858 <VIC>
A:Cross-references: GB:U31973; NID:g940230; PIDN:AAA96392.1; PID:g940231
A>Note: this sequence lacks a residue Tyr after the 231-Met, and has an additional resi
C:Genetics:
A:Gene: alpha'-pde
A:Introns: 160/3; 211/3; 241/3; 288/3; 313/3; 335/2; 357/3; 373/3; 423/3; 471/3; 494/3;
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide f
C:Keywords: cGMP binding; lipoprotein; phosphoric diester hydrolase; photoreceptor; pre
F:560-770/Domain: catalytic #status predicted <CAR>
F:561-794/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
F:855/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted

Query Match 15.4%; Score 758.5; DB 2; Length 858;
Best Local Similarity 25.8%; Pred. No. 66-41;
Matches 208; Conservative 151; Mismatches 299; Indels 147; Gaps 22;

QY 236 ELYDLDDASSLQIKVLYLQOE-----TQASRCLLIVS----- 268
Db 52 ELTQVEESALCLLELLWTVEEGTPEQGVHRAQLRALHLLQADRCMSFLCRSNGIPEVA 111
QY 269 -----EDNLQLSCRVIGDKVLEEEISFPLTTGRLGQGVVEDKKSQQLKDL--TS 314
Db 112 SRLLDVTPTSKPEDNL-----VGP---DKEVVPDLDIGVGAHAHTKTKHNVDPVKNS 162
QY 315 EDMQQLMSLGCVEQVAMLCVPVISRATDOVVALLACAFNKLGGDLFTDQDEHVIQHCFTY 374
Db 163 HPSDFMDKQTGYTVTKLLATPIV--VGKEVLAVIMAVNVKVASSEFSKQDEEVFSKYLNV 220
QY 375 STVLV---STLAFQKEOKLKCECQALLQVAKNLFTHLDDVSLQLEIITEARNLSNAETC 431
Db 221 SILRLHSTYMYNIESR---RSQILMWSANKVFEELTVERQPHKALYTVTRTYLNCERY 277
QY 432 SVFLLDQNELVAKVPDGGVW---EDES-----EIRI----- 460
Db 278 SIGLLDMTK-EKEFYDEWPVKLGEVEPYKPKTPDREVNPKYKIIDVILHGKEIKVPT 336
QY 461 -PAD-----OGIAGHVATTGQILNIPDAYA--HPLFYRGVDDSTGPRTRNLCPPIKNE 512
Db 337 PPADHWTLLISGLPTVVAENGFCNMLNAPADEYTFQKGPVDETGWIKNVLSPVNVKK 396
QY 513 QEVIGVABLNVKNGPFWFSKPEDLATAFSYCGISIAHSLLYKKNVQVRSHLANEMM 572
Db 337 EDIVGVATFYARKKQKPFDEHDEYITETLTQFLGWSLNTDTYKMKNKLENKRKDIAQEM 456
QY 573 MYHMKVSDDEYTKLH-----DGIQVAAI-----DSNFASFTYTPRSL 611
Db 457 MNQTKATPEEIKSILKFOEKLNVVDVDDCEBKQLVAILKEDLPDPRSAELYEFPSDFPL 516
QY 612 PEDDTSMAILSMQDMFNINNYKIDCPTLAFCLMVKGYRDPDPHYHNMHAFSVSHFCYL 671
Db 517 TEHGLIKGIRLFPFEINNVKFKPVEVLTWMTYTRKGYRAVTVYHNRHGFNVGTWFT 576
QY 672 LYKNLELTNYLEDMEI PALFTSCMCHDLDRGTNNNSFOVASKVLAALYSSSGSVMERHH 731
Db 577 LLMTGRKKYTYTDLFAFAMLAAPACHDIDHRGTNNLYQMKSTSPLARLHGS--SILERRH 634
QY 732 FAQAIATLNTHGCNIFDHSRKYQRMLDLMDRIILATDLAHLIRIFKDLQKMAE----- 786
Db 635 LEYSKTLQDSSNLIFQNLNKRQVETVHLFEVAILIATDLALYFKKRTMKQIVDACEQM 694
QY 787 -----VGYDRNTKQHSLLLCLLMTSCDLSQDKGWKTKTKIAELIYKEFPFSGDL 837
Db 695 QTEEBEAIKYTVDPDTKKE---IIMAMMTACDLSAITKPEVQSQVALLVANEFWEQGL 751
QY 838 EK-AMGNRPMEMMDREKA-VIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRH 895
Db 752 ERTVLQQQPIPMNDRNKKDELPLKQGVFIDPVCTFYVYKFSFRHKEITPMLSGLQNNRVE 811
QY 896 WTKVSHKFTIRGLPSNNSLDFLDEE 920
Db 812 WKSLADEYDAK-----MKVIEE 829

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RESULT 14
S13032
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) beta' chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S13032; S30763
R:Baehr, W.; Champagne, M.S.; Lee, A.K.; Pittler, S.J.
FEBS Lett. 278, 107-114, 1991
A:Title: Complete cDNA sequences of mouse rod photoreceptor cGMP phosphodiesterase alpha
  cing of the beta-subunit gene.
A:Reference number: S13030; MUID:91130581; PMID:1847109
A:Accession: S13032
A:Molecule type: DNA
A:Residues: 1-800 <BAE>
A:Cross-references: UNIPROT:Q62037; EMBL:X60133
R:Baehr, W.
submitted to the EMBL Data Library, June 1991
A:Reference number: S30762
A:Accession: S30763
A:Molecule type: DNA
A:Residues: 1-559,'R',561-800 <BA2>
A:Cross-references: GB:X87952; EMBL:X60133; PIDN:CAA61202.1; PID:9871433
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C:Keywords: alternative splicing; cGMP binding; phosphoric diester hydrolase
F:556-790/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match      15.4%; Score 756; DB 2; Length 800;
Best Local Similarity 27.4%; Pred. No. 7.8e-41;
Matches 212; Conservative 145; Mismatches 302; Indels 114; Gaps 22;

Qy 210 PEEAAGDQKG-----VAYTDQDRKILQCGELYD-LDASSLQKLVQYLOVQEQTQ 258
Db 29 PENVAGACEDGWLDCGSLRELQCVESAAFLVQDMQESVNNRERVFKILRLCTILH 88

Qy 259 ASRCLLVSDN--LQLSCKVIG---DKVLEE-----EISPLTTGRLGVQVEDKKS 306
Db 89 ADRCSLFVQRNGIAELATRLFSVQPDLSLEDCLVPPDSEIVPPLDIGIVGHVAQTKM 148

Qy 307 IQLKDLT-----SEMQQLQSMGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTD 361
Db 149 INVQDVARECPHFSPADLTDYV---TKNILLSTPMN--GRDVAVIMAVNKLDPGPCPTS 203

Qy 362 QDEHVIQCHFYTSVLTSLTFAFQEKQLKCEC---QALLQVAKNLFTHLDDVSVLLQEI 418
Db 204 EDEDVFTKYNFATNLK---IYHLSYLHNCETRRGQVLLSANKVFPELTDIERQFKA 260

Qy 419 ITEARNLSNABICSVFLDDQNELVAKVDFGGV---EDES----- 456
Db 261 FVTVRAYLNCERSYVGLLDMTK-EKEFFDVNPLMGEAQPSYGPRTPDGREIVFYKVIDY 319

Qy 457 -----ETRI-----PAD-----QGTAGHVTGQILNPIDAYNPL---FYRGVDDSTGFR 499
Db 320 ILHGKEDIKVIPTTPADHWALASGLPTTVABESGFTCNIMNASADMFENFQBGPLDDSGWV 379

Qy 500 TRNIIICFPKKNQSVIGVAELVNKINGPWFSEKDEDIATAFSIYCGISIAHSLLYKKVN 559
Db 380 IKNVLSMPLVNKKEEIGVGVATFYNRKQKPFDDQDEVLMESLTDFLGWSVLNTDTYDKN 439

Qy 560 BAQYRSHLANEMMYHMKVSDDEYTKLLHD---GIQFVAIDSNFA----- 602
Db 440 KLENRKDIAQDMVLVHVRCXDKDEIQEILPTRDLRGKEPADCEDELGKILKEELPGPTKF 499

Qy 603 ---SFTYTPRSLPEDDTSMAILSMQDMNFINNYKIDCPTLARCLVKKGYRDPDPYHNW 659
Db 500 DIYEFHFSDBLCTELELVKCGIQMYELGVGVKRFQIQEVLVRFVLSVSKAYRRTIYHNW 559

Qy 660 MHAFSVSHFCVLLYKNLELTWLEDMELFALFISCMCHDLDRGTNNNSFQVASKVLAAL 719
Db 560 GHGFNVAQTMFTLLMTGKLSYYTDLFAFMVATGLCHDIDHRGTNNLYQMKSNQPLAKL 619

Qy 720 YSSEGSVMRHHFAQAIILNTHGNCNIFDHSRKDYQRMGLMDRIILATDLAHLHRIFK 779
Db 620 HGS--SILERHHLFEGKFLAELSLNIYQNLNRRQHHEVHILMDIATIDALVYFKRT 677
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Qy 780 DLQKMAE-----VGVDRTNKQHSHLLCLLMTSCDLSDOTKGMKTKTKIAELIY 828
Db 678 MFQKIVDESRYVEDKKSWEYLSLETTKEILVMAMMTACDLSALTKEWEVQSKVALLVA 737

Qy 829 KEFFSQGDLEK-AMGNRPMEHMDREK-AYIPELQTSFMEHTAMPIYKLLQDLF 879
Db 738 AEFWEQGDLERTVLDQQPIPMWDRNKAELPKLVQGFIDFVCTFYVKEPLGIP 790

RESULT 15
S06418
3',5'-cyclic-GMP phosphodiesterase (EC 3.1.4.35) alpha chain - bovine
N:Alternate names: cGMP phosphodiesterase alpha chain
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: S06418; S27007; S00161; A34611; S08516
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Akhmedov, N.B.; Ishchenko, K.A.; Zha
T.M.; Bystrkov, N.S.; Severtsova, I.V.; Lipkin, V.M.
Dokl. Biochem. 296, 303-307, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S06418
A:Accession: S06418
A:Molecule type: mRNA
A:Residues: 1-859 <OVI>
A:Cross-references: UNIPROT:P11541; EMBL:X12756; NID:G616; PIDN:CAA31243.1; PID:G617
A:Accession: S27007
A:Molecule type: protein
A:Residues: 2-11;22-27;32-40;95-98;112-115;180-193;248-267;275-282;297-306;312-330;361-3
645;654-661;663-667;703-712;734-736;751-760;766-771;787-798;811-819 <OVG>
A:Note: This paper is a translation of the Russian paper published in Dokl. Akad. Nauk S
R:Ovchinnikov, Y.A.; Gubanov, V.V.; Khramtsov, N.V.; Ischenko, K.A.; Zagranichny, V.E.;
FEBS Lett. 223, 169-173, 1987
A:Title: Cyclic GMP phosphodiesterase from bovine retina. Amino acid sequence of the alp
A:Reference number: S00161; MUID:88030033; PMID:2822478
A:Accession: S00161
A:Molecule type: mRNA
A:Residues: 1-859 <OV2>
A:Cross-references: EMBL:M27541; NID:G162826; PIDN:AAA30441.1; PID:G162828
A:Note: part of this sequence was confirmed by protein sequencing
R:Pittler, S.J.; Baehr, W.; Wasemuth, J.J.; McConnell, D.G.; Champagne, M.S.; vanTuinen,
Genomics 6, 272-283, 1990
A:Title: Molecular characterization of human and bovine rod photoreceptor cGMP phosphodi
A:Reference number: A34611; MUID:90169986; PMID:2155175
A:Accession: A34611
A:Molecule type: mRNA
A:Residues: 1-193,'V',195-423,'T',425-674,'P',676-859 <PIT>
A:Cross-references: GB:M26043; NID:G162833; PIDN:AAA30443.1; PID:G162834
C:Comment: This protein is involved in the transduction and amplification of the visual
C:Superfamily: 3',5'-cyclic-GMP phosphodiesterase alpha chain; 3',5'-cyclic-nucleotide p
C:Keywords: acetylated amino end; cGMP; heterotrimer; phosphoric diester hydrolase; reti
F:2-859/Product: 3',5'-cyclic-GMP phosphodiesterase alpha chain #status experimental <MA
F:558-791/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F:2/Modified site: acetylated amino end (Gly) (in mature form) #status experimental

Query Match      15.3%; Score 753.5; DB 1; Length 859;
Best Local Similarity 26.1%; Pred. No. 1.3e-40;
Matches 217; Conservative 150; Mismatches 349; Indels 115; Gaps 24;

Qy 210 PEEAAGDQKG--GVAYTDQDRKILQCGELYD-LDASSLQKLVQYLOQEQTSRCCLLL 266
Db 39 PREAAVDFSNYHALNSVEESEIIFDLRLDFQDNLOAEKCVFNVMKKLCLFLQADRMSLFM 98

Qy 267 VSEDN--LQLSCKVIG---DKVLEE-----EISFPLTTGRLGVQVEDKKSILQKDLTS 314
Db 99 YRARNGIAELATRLFNHVKDAVLECLVAPDSEIVFPLDMGVGVHVALSKIVNVPN-TE 157

Qy 315 ED---MQQLQSMGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFTDDEHVIQCHCF 371
Db 158 EDEHCFDVPDTLTETVQTKNILASPIMN--GKDVVAIIMAVNKNVDPGPHFTEDEILLKYL 215

Qy 372 HVTSTVLSTLTFQKEQKLKCEC---QALLQVAKNLFTHLDDVSVLLQELIITEARNLSNA 428
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:06:11 ; Search time 117.813 Seconds
(without alignments)
3092.423 Million cell updates/sec

Title: US-10-697-894-43
Perfect score: 4911
Sequence: 1 MGQACGHSILCRSQYPAAR.....VPLDGRAPINGCCSLDAE 942

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4911	100.0	942	2	AAR69728 Cyclic-GM
2	4911	100.0	942	2	Aaw11239 Cyclic GM
3	4911	100.0	942	2	Aaw18049 cGS-PDE a
4	4911	100.0	942	2	Aaw71225 Bovine br
5	4911	100.0	942	2	Aaw77041 Cyclic-GM
6	4911	100.0	942	2	Aaw60753 cGS-PDE 1
7	4911	100.0	942	3	Aay80985 Bovine br
8	4911	100.0	942	6	ABU58724 Bovine br
9	4911	100.0	942	8	ADQ94963 Bovine cG
10	4871	99.2	942	2	AAR28408 CGS PDE f
11	4728.5	96.3	941	2	AAR69729 Cyclic-GM
12	4728.5	96.3	941	2	Aaw11253 pHC96n c
13	4728.5	96.3	941	2	Aaw18050 Human cgs
14	4728.5	96.3	941	2	Aaw71226 Human cgs
15	4728.5	96.3	941	2	Aaw77042 Cyclic-GM
16	4728.5	96.3	941	2	Aaw60754 Human cyc
17	4728.5	96.3	941	3	Aay80986 Human cgs
18	4728.5	96.3	941	4	Aae07954 Human pho
19	4728.5	96.3	941	4	AAB507918 Human pho
20	4728.5	96.3	941	4	AAB85117 Human cgm
21	4728.5	96.3	941	4	AAB85106 Human cgm
22	4728.5	96.3	941	4	AAG66539 Human int
23	4728.5	96.3	941	6	ABU58725 Human bra
24	4728.5	96.3	941	7	ADD14154 Human src
25	4728.5	96.3	941	7	ADe62314 Human Pro

26	4728.5	96.3	941	8	ADO21792	Ado21792 Human pho
27	4728.5	96.3	941	8	ADQ94965	Adq94965 Plasmid p
28	4690.5	95.5	941	2	AAR28409	Aar28409 Human foe
29	4657	94.8	921	2	AAR69727	Aar69727 Cyclic-GM
30	4657	94.8	921	2	AAW11252	AAW11252 Clone p3C
31	4657	94.8	921	2	AAW18048	AAW18048 Cyclic-GM
32	4657	94.8	921	2	AAW71224	AAW71224 cGS-PDE e
33	4657	94.8	921	2	AAW77040	AAW77040 Adrenal c
34	4657	94.8	921	2	AAW60752	AAW60752 cGS-PDE i
35	4657	94.8	921	3	AAy80984	Aay80984 Bovine ad
36	4657	94.8	921	6	ABU58723	Abu58723 Bovine ad
37	4657	94.8	921	8	ADQ94959	Adq94959 Bovine p3
38	4640	94.5	921	2	AAR28407	Aar28407 cGS-PDE f
39	4480.5	91.2	920	6	ABR54205	ABr54205 Human NOV
40	4474.5	91.1	920	5	AAQ15507	AAQ15507 Human pho
41	4474.5	91.1	920	5	ABG70998	ABg70998 Human pho
42	4418	90.0	928	7	ADe62312	AdE62312 Rat Prote
43	4272.5	87.0	950	7	ADM04243	Adm04243 Human pro
44	3484.5	71.0	786	7	ADB64790	ADB64790 Human pro
45	3345	68.1	685	8	ADR10446	ADR10446 Human pro

ALIGNMENTS

RESULT 1
AAR69728
ID AAR69728 standard; protein; 942 AA.
XX AC AAR69728;
XX DT 25-MAR-2003 (revised)
DT 11-OCT-1995 (first entry)
XX DE Cyclic-GMP stimulated nucleotide PDE clone pBBCGSPDE-7.
XX KW Cyclic-GMP stimulated nucleotide phospho-diesterase; antibodies;
KW bovine adrenal cortex; hormones; neurotransmitters;
KW transmission regulation; enzyme purification; clone pBBCGSPDE-7.
XX OS Bos taurus.
XX PN US5389527-A.
XX PD 14-FEB-1995.
XX PF 20-APR-1992; 92US-00872644.
XX PR 19-APR-1991; 91US-00688356.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Sonnenburg WK, Charbonneau H, Beavo JA;
PI WPI; 1995-090205/12.
XX DR N-PSDB; AAQ83977.
XX PT New nucleic acid encoding cyclic-GMP stimulated nucleotide phospho-diesterase - and related vectors and transformed cells, useful for screening cpds. for phospho-diesterase modulating activity.
XX PS Example 5; Col 79-86; 69pp; English.
XX CC AAQ83977 encodes AAR69728 the bovine brain cyclic-GMP stimulated nucleotide phospho-diesterase (Cam PDE) clone pBBCGSPDE-7. Eukaryotic cells that express Cam PDE can be used to screen cpds. for the ability to modulate Cam PDE activity. Cam PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers. Antibodies raised against Cam PDE can be used for enzyme purificn., or determination.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 942 AA;

```
Query Match      100.0%; Score 4911; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1  MQACGHSILCRSQOYPAARPAERPGQOVFLKPDPPPPPCADSLQDALLSLGSDIVD 60
Db 1  MQACGHSILCRSQOYPAARPAERPGQOVFLKPDPPPPPCADSLQDALLSLGSDIVD 60

QY 61  AGLOQAVKEALSAVLPKVTETVYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN 120
Db 61  AGLOQAVKEALSAVLPKVTETVYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN 120

QY 121  GLGPSDLPGKPLARLAPLAPDPTQVLPVLDKEAGAAVAVILVHCQGLSNEEWSLOAV 180
Db 121  GLGPSDLPGKPLARLAPLAPDPTQVLPVLDKEAGAAVAVILVHCQGLSNEEWSLOAV 180

QY 181  EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240
Db 181  EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQLCGELYDL 240

QY 241  DASSLQLKVLQYLOQETOASRCCLLLVSEDNLQLSKVIGDKVLEBESFPPLTTGRLGQV 300
Db 241  DASSLQLKVLQYLOQETOASRCCLLLVSEDNLQLSKVIGDKVLEBESFPPLTTGRLGQV 300

QY 301  VEDKKSIGLQDLTSEDMOQLSMLGCEVOQMLCVPISRATDQVVALACAFNKGGLDFT 360
Db 301  VEDKKSIGLQDLTSEDMOQLSMLGCEVOQMLCVPISRATDQVVALACAFNKGGLDFT 360

QY 361  DQDEHVIQCHFYHTSVLTSTLAFQEKQLKCECQALLQVAKNLFTHLDDVSVLLQEIT 420
Db 361  DQDEHVIQCHFYHTSVLTSTLAFQEKQLKCECQALLQVAKNLFTHLDDVSVLLQEIT 420

QY 421  EARNLSNAEICSVFLLDQNELVAKVFDGSGVEDESYEIRIPADQGIAGHVATTGQILNIP 480
Db 421  EARNLSNAEICSVFLLDQNELVAKVFDGSGVEDESYEIRIPADQGIAGHVATTGQILNIP 480

QY 481  DAYAHLFVRGVDDSTGFRNLCFPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATA 540
Db 481  DAYAHLFVRGVDDSTGFRNLCFPPIKNEQEVIGVAELVNKINGPWFSEKDEDLATA 540

QY 541  FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGPVAADSN 600
Db 541  FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIGPVAADSN 600

QY 601  FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYHNWM 660
Db 601  FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPYHNWM 660

QY 661  HAFSVSHFCYLLYKNLELTYLDEMEIFALFTSCMCHDLHRTGNTNSFOVASKSVLAALY 720
Db 661  HAFSVSHFCYLLYKNLELTYLDEMEIFALFTSCMCHDLHRTGNTNSFOVASKSVLAALY 720

QY 721  SSEGSVMERHFAQAIALINTHGNCIFDHFSRKDYQRMLDLMDRIILATDLAHLRIKFD 780
Db 721  SSEGSVMERHFAQAIALINTHGNCIFDHFSRKDYQRMLDLMDRIILATDLAHLRIKFD 780

QY 781  LQKMAEVGYDRTNKQHSLLCLLMTSCDLSDQTKGWKTKRIABLIYKEFPFSGDLEKA 840
Db 781  LQKMAEVGYDRTNKQHSLLCLLMTSCDLSDQTKGWKTKRIABLIYKEFPFSGDLEKA 840

QY 841  MGNRPMEMWMDREKAVIPELOJFSEMEHIAMPYIKLQDLFPKAAELYERVA NRHWTKVS 900
Db 841  MGNRPMEMWMDREKAVIPELOJFSEMEHIAMPYIKLQDLFPKAAELYERVA NRHWTKVS 900

QY 901  HKFTIRGLPSNNSLDFLDEEYEVPLDGCARAPINGCCSIDAE 942
Db 901  HKFTIRGLPSNNSLDFLDEEYEVPLDGCARAPINGCCSIDAE 942
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RESULT 2
AAW11239
ID AAW11239 standard; protein; 942 AA.

```
XX AAW11239;
XX AC
XX 25-MAR-2003 (revised)
XX 17-MAR-1997 (first entry)
XX DT
XX Cyclic GMP stimulated phosphodiesterase.
XX DE
XX Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP;
XX KW adrenal gland; cGMP; transmembrane signal; extracellular hormone;
XX KW neurotransmitter; antibody.
XX OS
XX Bos taurus.
XX FN
XX US5580771-A.
XX PD
XX 03-DEC-1996.
XX PP
XX 29-AUG-1994; 94US-00297494.
XX PR
XX 19-APR-1991; 91US-00688356.
XX PR 20-APR-1992; 92US-00872644.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Charbonneau H, Sonnenburg WK, Beavo JA;
XX WPI; 1997-033573/03.
XX DR N-PSDB; AAT51090.
XX PT
XX DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
XX recombinant enzyme.
XX PS Claim 1; Col 77-86; 69pp; English.
XX CC This sequence represents the cyclic GMP stimulated phosphodiesterase (cGS
CC -PDE) clone pBGCSPDE-5 isolated from bovine brain. This sequence is
CC nearly identical to the bovine adrenal gland cGS-PDE isozyme. The cyclic
CC nucleotide phosphodiesterases (PDEs) catalyze the hydrolysis of 3',5'-
CC cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'-
CC nucleotide monophosphates. The PDEs are therefore important in the
CC control of the cellular concentration of cyclic nucleotides. The PDEs
CC are, in turn, regulated by transmembrane signals or second messenger
CC ligands such as calcium ion or cGMP. The PDEs therefore have a central
CC role in regulating the flow of information from extracellular hormones,
CC neurotransmitters, or other signals that use the cyclic nucleotides as
CC messengers. PDEs are present in most of the cells and tissues of
CC eukaryotic organisms, but only in trace amounts. cGS-PDEs are stimulated
CC by cGMP in effecting cAMP hydrolysis. This is thought to occur through a
CC noncatalytic cGMP-specific site present on the cGS-PDE. The DNA encoding
CC this sequence can be used for the production of recombinant cGS-PDE,
CC which may have therapeutic and diagnostic uses. This sequence may also be
CC useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX SQ
```

Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1  MQACGHSILCRSQOYPAARPAERPGQOVFLKPDPPPPPCADSLQDALLSLGSDIVD 60
Db 1  MQACGHSILCRSQOYPAARPAERPGQOVFLKPDPPPPPCADSLQDALLSLGSDIVD 60

QY 61  AGLOQAVKEALSAVLPKVTETVYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN 120
Db 61  AGLOQAVKEALSAVLPKVTETVYTYLLDGSRLVCEPPHELPOBQKREAVISRRLGCN 120

QY 121  GLGPSDLPGKPLARLAPLAPDPTQVLPVLDKEAGAAVAVILVHCQGLSNEEWSLOAV 180
Db 121  GLGPSDLPGKPLARLAPLAPDPTQVLPVLDKEAGAAVAVILVHCQGLSNEEWSLOAV 180
```

QY 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAGDQKGGVAYTDDQDKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAGDQKGGVAYTDDQDKILQLCGELYDL 240
QY 241 DASSLQLKVLQYLOQOQTOASRCCLLVSDNLQSKVIGDKVLEEEISFPPLTTGRLGV 300
Db 241 DASSLQLKVLQYLOQOQTOASRCCLLVSDNLQSKVIGDKVLEEEISFPPLTTGRLGV 300
QY 301 VEDKKSILQKDLTSDMQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSDMQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQHCFTHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQDEHVIQHCFTHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSEDEDLATA 540
Db 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSEDEDLATA 540
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
QY 601 PASFTYTPRSLPDDTSMALLSMLQDMNFTNNYKIDCPTLARECLMVKKGYRDPVYHNM 660
Db 601 PASFTYTPRSLPDDTSMALLSMLQDMNFTNNYKIDCPTLARECLMVKKGYRDPVYHNM 660
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALY 720
Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALY 720
QY 721 SSEGSMERHFAQAIATLNTGNCNIPDFHSRKYQYRMOLDLRDIILATDLAHLRIKFD 780
Db 721 SSEGSMERHFAQAIATLNTGNCNIPDFHSRKYQYRMOLDLRDIILATDLAHLRIKFD 780
QY 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSDQTKGKWTTRKIAELIYKEFFSQGDLEKA 840
Db 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSDQTKGKWTTRKIAELIYKEFFSQGDLEKA 840
QY 841 MGNRRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 841 MGNRRPMEMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
QY 901 HKFTIRGLPSNNSLDPLDEEYVPLDGDARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDPLDEEYVPLDGDARAPINGCCSLDAE 942

RESULT 3

AAW18049
ID AAW18049 standard; protein; 942 AA.
XX
AC AAW18049;
XX
DT 25-MAR-2003 (revised)
DT 05-AUG-1997 (first entry)
XX

cGS-PDE amino acid sequence from the pBBCGSPDE-7 insert.

XX Cyclic-GMP-stimulated phosphodiesterase; antibody; cow;
KW polymerase chain reaction.
XX

OS Bos taurus.

XX US5602019-A.

XX 11-FEB-1997.

XX

PF 29-AUG-1994; 94US-00297510.
XX
PR 19-APR-1991; 91US-00688356.
PR 20-APR-1992; 92US-00872644.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
XX
DR WPI; 1997-131799/12.
DR N-PSDB; AAT67223.
XX
PT DNA encoding bovine and human phosphodiesterase enzymes - stimulated by
PT calcium/calmodulin, useful for recombinant prodn. of the enzymes.
XX
PS Example 5; Col 85-92; 69pp; English.
XX
CC The present sequence represents the pBBCGSPDE-7 bovine brain insert amino
CC acid sequence. The large open reading frame encodes a 942-residue
CC polypeptide that is nearly identical to the adrenal gland cyclic-GMP-
CC stimulated phosphodiesterase (cGS-PDE) isozyme. The difference in the
CC primary structure of the two isozymes lies in the amino-terminal residues
CC 1-46 of the brain cGS-PDE, and residues 1-25 of the adrenal cGS-PDE. The
CC remaining carboxy-terminal residues in both are identical. The DNA
CC sequences of the cGS-PDE's are used for the production of the recombinant
CC enzymes, which in turn may be used for antibody production and to screen
CC for compounds that modulate phosphodiesterase activity. (Updated on 25-
CC MAR-2003 to correct Pf field.) (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 942 AA;
Query Match 100.0%; Score 4911; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQQACGHSILCSQQYPAARPAEPRGQQVFLKDPDPPPPPPQCADSLQALLSLGSLVIDV 60
Db 1 MQQACGHSILCSQQYPAARPAEPRGQQVFLKDPDPPPPPPQCADSLQALLSLGSLVIDV 60
QY 61 AGLOQAVKEALSAVLPKVETVYTLDDGESRLVCEPPHELPOEGKVRSAVSRKRLGCV 120
Db 61 AGLOQAVKEALSAVLPKVETVYTLDDGESRLVCEPPHELPOEGKVRSAVSRKRLGCV 120
QY 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAIVLHCGQLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAIVLHCGQLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAGDQKGGVAYTDDQDKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEEAGDQKGGVAYTDDQDKILQLCGELYDL 240
QY 241 DASSLQLKVLQYLOQOQTOASRCCLLVSDNLQSKVIGDKVLEEEISFPPLTTGRLGV 300
Db 241 DASSLQLKVLQYLOQOQTOASRCCLLVSDNLQSKVIGDKVLEEEISFPPLTTGRLGV 300
QY 301 VEDKKSILQKDLTSDMQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSDMQQLQSMGLCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQHCFTHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQDEHVIQHCFTHTSTVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSEDEDLATA 540
Db 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSEDEDLATA 540
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600

541 FSIYCGISIAHSLYKKNVQAQRSHLANEMMYHMKVSDDEYTKLHDGILQPVAAIDSN 600
 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNM 660
 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNM 660
 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720
 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720
 721 SSEGSMERHHAFAQAIATLNTGNCNIFDHSRKYQRMMLDMRDIIATDLAHLRIKPD 780
 721 SSEGSMERHHAFAQAIATLNTGNCNIFDHSRKYQRMMLDMRDIIATDLAHLRIKPD 780
 781 LQKMAEYGYDRNKKQHSLILCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
 781 LQKMAEYGYDRNKKQHSLILCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
 841 MGNRPMEHMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
 841 MGNRPMEHMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
 901 HKFTIRGLPSNNSLDLDEEYVDPDLCGARAPINGCCSLDAE 942
 901 HKFTIRGLPSNNSLDLDEEYVDPDLCGARAPINGCCSLDAE 942

RESULT 4

AA711225
 ID AA711225 standard; protein; 942 AA.
 XX
 AC AA711225;
 XX
 DT 29-OCT-1998 (first entry)
 XX
 DE Bovine brain CGS-PDE sequence of clone pBBCGSPDE-7.
 XX
 KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; Cam-PDE;
 KW assay; identification; modification; enzymatic activity; modulator;
 KW cyclic guanosine monophosphate-stimulated phosphodiesterase; CGS-PDE.
 XX
 OS Bos sp.
 XX
 XX US5800987-A.
 XX
 PD 01-SEP-1998.
 XX
 PF 31-MAY-1995; 95US-00455525.
 XX
 PR 19-APR-1991; 91US-00688356.
 PR 20-APR-1992; 92US-00872644.
 PR 29-AUG-1994; 94US-00297494.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;
 XX
 DR WPI; 1998-494762/42.
 XX
 PT Identification of modulators of Calcium/calmodulin sensitive cyclic
 PT nucleotide phosphodiesterase - uses recombinant cells expressing the
 PT enzyme and monitoring protein expression in the presence of potential
 PT modulators.
 XX
 PS Example 5; Col 85-90; 69pp; English.
 XX
 CC The present sequence is encoded by the DNA sequence of clone pBBCGSPDE-7,
 CC isolated from bovine brain. This clone encodes cyclic guanosine
 CC monophosphate-stimulated phosphodiesterase (CGS-PDE) cDNA. The
 CC specification also describes Ca2+/calmodulin sensitive cyclic nucleotide
 CC phosphodiesterase (Cam-PDE) enzymes. Cam-PDE enzymes catalyze the
 CC hydrolysis of cyclic nucleotides and as such control their intracellular

CC level. They are controlled by second messengers e.g. Ca2+ and calmodulin
 CC and transmembrane signals and through pathways involving these, regulate
 CC flow of information from extracellular hormones, neurotransmitters and
 CC other signals using cyclic nucleotides as messengers. The specification
 CC describes an assay for identifying a chemical agent which modifies the
 CC enzymatic activity of a mammalian Cam-PDE. The assays are useful for
 CC identifying modulators of Cam-PDEs. The assay is carried out by
 CC incubating cells expressing Cam-PDE with the suspected modulator and
 CC measuring its effect e.g. monitoring the hydrolysis of cAMP and/or CGMP
 XX
 SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 2; Length 942;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MQQACGHSILCRSQQYPAARPAEPGRQQVFLKPBEPDPPOPCADSLQDALLSLGSDIV 60
 Db 1 MQQACGHSILCRSQQYPAARPAEPGRQQVFLKPBEPDPPOPCADSLQDALLSLGSDIV 60
 Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEEPHELPOEGKREAVISRKLGN 120
 Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEEPHELPOEGKREAVISRKLGN 120
 Qy 121 GLGPSDLPGKPLARLVAAPDQVLPVLDKEGAAVAAVILVHCGQLSNEEWSLOAV 180
 Db 121 GLGPSDLPGKPLARLVAAPDQVLPVLDKEGAAVAAVILVHCGQLSNEEWSLOAV 180
 Qy 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDKRILQLCGELYDL 240
 Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQKGVAYTDQDKRILQLCGELYDL 240
 Qy 241 DASSLQLKVLQYLOQETQASRCCILLVSEDNLQLSCKVIGDKVLEEEISPLTTGRLQGV 300
 Db 241 DASSLQLKVLQYLOQETQASRCCILLVSEDNLQLSCKVIGDKVLEEEISPLTTGRLQGV 300
 Qy 301 VEDKKSITQLKDLTSEDMMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKGGLFT 360
 Db 301 VEDKKSITQLKDLTSEDMMQQLQSMGCEVQAMLCVPVISRATDQVVALACAFNKGGLFT 360
 Qy 361 DQDEHVIQCHFHVTSTVLTSTLAFQKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 420
 Db 361 DQDEHVIQCHFHVTSTVLTSTLAFQKQKCECOALLQVAKNLFTHLDDVSVLLQEIIT 420
 Qy 421 EARLNSNAEICSVELLDQNELVAKVFDGGVDESEYRIRIPADQGIAGHVATTGQILNIP 480
 Db 421 EARLNSNAEICSVELLDQNELVAKVFDGGVDESEYRIRIPADQGIAGHVATTGQILNIP 480
 Qy 481 DAYAHPFYRGVDDSTGFRTRNIIICFPICKENQEVIGVAELVNKINGPWFSKFDBDLATA 540
 Db 481 DAYAHPFYRGVDDSTGFRTRNIIICFPICKENQEVIGVAELVNKINGPWFSKFDBDLATA 540
 Qy 541 FSIYCGISIAHSLYKKNVQAQRSHLANEMMYHMKVSDDEYTKLHDGILQPVAAIDSN 600
 Db 541 FSIYCGISIAHSLYKKNVQAQRSHLANEMMYHMKVSDDEYTKLHDGILQPVAAIDSN 600
 Qy 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNM 660
 Db 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPYHNM 660
 Qy 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720
 Db 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFTSCMCHDLDRGTNNSFQVASKSVLAALY 720
 Qy 721 SSEGSMERHHAFAQAIATLNTGNCNIFDHSRKYQRMMLDMRDIIATDLAHLRIKPD 780
 Db 721 SSEGSMERHHAFAQAIATLNTGNCNIFDHSRKYQRMMLDMRDIIATDLAHLRIKPD 780
 Qy 781 LQKMAEYGYDRNKKQHSLILCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
 Db 781 LQKMAEYGYDRNKKQHSLILCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
 Qy 841 MGNRPMEHMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 900

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Db      841  ||||||| 901  ||||||| 901  ||||||| 900
      MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS
Qy      901  HKFTIRGLPSNNSLDFLDEBEYEPDLGAPINGCCSLDAE 942
      |||||||
Db      901  HKFTIRGLPSNNSLDFLDEBEYEPDLGAPINGCCSLDAE 942
      |||||||

RESULT 5
AAW77041
ID  AAW77041 standard; protein; 942 AA.
XX
AC  AAW77041;
XX
DT  09-NOV-1998 (first entry)
DE  Cyclic-GMP-stimulated phosphodiesterase clone pBBCGSPDE-7.
XX
KW  Cow; Ca2+ stimulated phosphodiesterase;
KW  Calmodulin stimulated phosphodiesterase; therapeutic; antibody.
XX
OS  Bos sp.
XX
XX  US5789553-A.
XX
XX  04-AUG-1998.
XX
XX  31-MAY-1995; 95US-00455526.
XX
XX  19-APR-1991; 91US-00688356.
XX  20-APR-1992; 92US-00872644.
XX  29-AUG-1994; 94US-00297494.
XX
XX  (UNIW ) UNIV WASHINGTON.
XX
XX  Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;
XX  WPI; 1998-446185/38.
XX  N-PSDB; AAV48204.
XX
XX  Antibody to phosphodiesterase polypeptide - useful for purification or
XX  detection of polypeptide.
XX
XX  Example 5; Column 77/86; 68pp; English.
XX
XX  The cyclic-GMP-stimulated phosphodiesterase clone pBBCGSPDE-7 from the
XX  bovine brain, is one of several phosphodiesterases isolated in this
XX  invention. The phosphodiesterases were used to transform host cells,
XX  preferably mammalian or yeast cells. The recombinant proteins and
XX  fragments produced can be used for therapeutic, diagnostic, and
XX  prognostic purposes and will provide the basis for preparation of
XX  monoclonal and polyclonal antibodies. An antibody specific for the
XX  Ca2+/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE)
XX  polypeptide is useful for affinity purification or detection of the
XX  polypeptide and is selective only for the Ca2+/calmodulin stimulated
XX  cyclic nucleotide PDE polypeptide
XX
SQ  Sequence 942 AA;

Query Match      100.0%; Score 4911; DB 2; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MQQACGHSILCRSQQYPAARPAEPGQQVFLKPDPPPPPCADSLQDALLSLGSVIDV 60
Db      1  MQQACGHSILCRSQQYPAARPAEPGQQVFLKPDPPPPPCADSLQDALLSLGSVIDV 60
Qy      61  AGLQAVKEALSAVLPKVETVTVTYLLDGSRLVCEPPELHPQEGKVREAVISRKLGCN 120
Db      61  AGLQAVKEALSAVLPKVETVTVTYLLDGSRLVCEPPELHPQEGKVREAVISRKLGCN 120
Qy      121  GLGPSDDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180
      |||||||
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Db      121  GLGPSDDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEWSLQAV 180
Qy      181  EXHTLVALKRVQALQORESSVAPEATQNPPEAAGQKGGVAYTDDQRKILQCGELYDL 240
      |||||||
Db      181  EXHTLVALKRVQALQORESSVAPEATQNPPEAAGQKGGVAYTDDQRKILQCGELYDL 240
      |||||||
Qy      241  DASSLQLKVLQYLQOETQASRCCLLLVSEDNLQLSCKVI GDKVLEEEISFPLTTGRLQV 300
      |||||||
Db      241  DASSLQLKVLQYLQOETQASRCCLLLVSEDNLQLSCKVI GDKVLEEEISFPLTTGRLQV 300
      |||||||
Qy      301  VEDKKSIOQLKDLTSEDNQMLGCEVOAMLCVPVISRATDOVVALACAFNKLGGDLFT 360
      |||||||
Db      301  VEDKKSIOQLKDLTSEDNQMLGCEVOAMLCVPVISRATDOVVALACAFNKLGGDLFT 360
      |||||||
Qy      361  DQDEHVIQHCFTYTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT 420
      |||||||
Db      361  DQDEHVIQHCFTYTSVLTSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLLQEIT 420
      |||||||
Qy      421  EARNLSNAEICSVFLLDQNELVAKVFDGGVVESEYEIRIPADOGIAGHVATTGQILNIP 480
      |||||||
Db      421  EARNLSNAEICSVFLLDQNELVAKVFDGGVVESEYEIRIPADOGIAGHVATTGQILNIP 480
      |||||||
Qy      481  DAYAHPLFYRGVDDSTGPRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSKFDEDLATA 540
      |||||||
Db      481  DAYAHPLFYRGVDDSTGPRTRNLCFPIKNENQEVIGVAELVKNKINGPWFSKFDEDLATA 540
      |||||||
Qy      541  FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
      |||||||
Db      541  FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
      |||||||
Qy      601  PASFTYTPRSLPEDDTSMAILSNLQDMNFNNYKIDCPTLARFCLMVKGYRDPPTNNWM 660
      |||||||
Db      601  PASFTYTPRSLPEDDTSMAILSNLQDMNFNNYKIDCPTLARFCLMVKGYRDPPTNNWM 660
      |||||||
Qy      661  HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
      |||||||
Db      661  HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
      |||||||
Qy      721  SSEGSVMERHHPAQAIILNTHGCNI FOHFSRKDYQRMLDLMDRIILATDLAHLRI FKD 780
      |||||||
Db      721  SSEGSVMERHHPAQAIILNTHGCNI FOHFSRKDYQRMLDLMDRIILATDLAHLRI FKD 780
      |||||||
Qy      781  LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTGKGTTRKIAELIYKEFFSQGDLKA 840
      |||||||
Db      781  LQKMAEVGYDRTNKHSHLLCLLMTSCDLSQDTGKGTTRKIAELIYKEFFSQGDLKA 840
      |||||||
Qy      841  MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
      |||||||
Db      841  MGNRPMMMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
      |||||||
Qy      901  HKFTIRGLPSNNSLDFLDEBEYEPDLGAPINGCCSLDAE 942
      |||||||
Db      901  HKFTIRGLPSNNSLDFLDEBEYEPDLGAPINGCCSLDAE 942
      |||||||

RESULT 6
AAW60753
ID  AAW60753 standard; protein; 942 AA.
XX
AC  AAW60753;
XX
DT  07-SEP-1998 (first entry)
XX
XX  CGS-PDE isolated from bovine brain.
XX
XX  Bovine; decrease; intracellular concentration; CAMP; cGMP;
XX  calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterase;
XX  CaM-PDE; therapy; prognosis; diagnosis; specific modulator;
XX  CaM-PDE activity; identification; signalling; extracellular hormone;
XX  neurotransmitter; selective inhibitor; cardiotonic; antidiuretic;
XX  antihypertensive; antithrombotic agent; cGS-PDE.
XX  cyclic-GMP-nucleotide phosphodiesterase; cGS-PDE.
XX
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OS Bos sp.
 XX US5776752-A.
 XX
 XX
 PD 07-JUL-1998.
 XX
 XX 07-JUN-1995; 95US-00479532.
 XX
 PR 19-APR-1991; 91US-00688356.
 PR 20-APR-1992; 92US-00872644.
 PR 29-AUG-1994; 94US-00297494.
 XX
 XX (UNIW) UNIV WASHINGTON.
 XX
 XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
 XX
 DR WPI; 1998-398038/34.
 DR N-PSDB; AAV36156.
 XX
 XX New calmodulin and calcium stimulated cyclic nucleotide phosphodiesterase
 PT - used e.g to identify selective modulators, potentially useful as e.g.
 PT cardiotonic, antidepressant, antihypertensive agents.
 XX
 XX Example 5; Col 85-90; 69pp; English.
 XX
 CC The present sequence represents cyclic-GMP-nucleotide phosphodiesterase
 CC (cGS-PDE), and is isolated from bovine. The specification describes
 CC calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterases
 CC (Cam-PDEs). Cam-PDEs are characterised by their responsiveness to
 CC intracellular calcium, which leads to a decreased intracellular
 CC concentration of cAMP and/or cGMP. Cam-PDEs, and their fragments or
 CC synthetic peptides, are used in therapy, prognosis and diagnosis. They
 CC are also used to generate specific antibodies useful as immunoassay
 CC reagents for detecting the protein or for affinity purification and for
 CC identifying specific modulators of Cam-PDE activity. Cam-PDEs are
 CC implicated in signalling involving extracellular hormones and
 CC neurotransmitters, so selective inhibitors are potentially useful as
 CC cardiotonic, antidepressant, antihypertensive and antithrombotic agents
 XX
 XX SQ Sequence 942 AA;
 Query Match 100.0%; Score 4911; DB 2; Length 942;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MGQACGHSILCRSQYPAARPAEPGRGQVFLKPDPEPPPPQPCADSLQDALLSLGSLVIDV 60
 Db 1 MGQACGHSILCRSQYPAARPAEPGRGQVFLKPDPEPPPPQPCADSLQDALLSLGSLVIDV 60
 Qy 61 AGLOQAVKEALSVALPKVETVYTYLLDGSRLVCEPPHELPOEGKVREAVISRKLGCN 120
 Db 61 AGLOQAVKEALSVALPKVETVYTYLLDGSRLVCEPPHELPOEGKVREAVISRKLGCN 120
 Qy 121 GLGPSDLPGKPLARLAVLAPDPTQVLPVLDKEAGAAVILVHCGQLSNEWSLQAV 180
 Db 121 GLGPSDLPGKPLARLAVLAPDPTQVLPVLDKEAGAAVILVHCGQLSNEWSLQAV 180
 Qy 181 EKHTLVALKRYVALQQRSSVAPETQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL 240
 Db 181 EKHTLVALKRYVALQQRSSVAPETQNPPEEAAGDQKGGVAYTDQDRKILQLCGELYDL 240
 Qy 241 DASSLQLKVLQYLOEQTAQSCCLLLVSEDNLQJLCKVIGDKVLEEBISFPFLTTGRLGQV 300
 Db 241 DASSLQLKVLQYLOEQTAQSCCLLLVSEDNLQJLCKVIGDKVLEEBISFPFLTTGRLGQV 300
 Qy 301 VEDKKSIOQLKDLTSEDMOQLSMLGCEVQAMLCVPVTSRATDQVVALACAFNKLGGLFT 360
 Db 301 VEDKKSIOQLKDLTSEDMOQLSMLGCEVQAMLCVPVTSRATDQVVALACAFNKLGGLFT 360
 Qy 361 DQDEHVIGHCFHYTSTVLSTLAFQKEQKJLCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
 Db 361 DQDEHVIGHCFHYTSTVLSTLAFQKEQKJLCEQALLQVAKNLFTHLDDVSVLLQEIIT 420

Qy 421 EARNLSNAEICSVELLDQNELVAKVFDGGVVEDESYEIRIPADOGIAGHVATTGQILNIP 480
 Db 421 EARNLSNAEICSVELLDQNELVAKVFDGGVVEDESYEIRIPADOGIAGHVATTGQILNIP 480
 Qy 481 DAYAHPFLFYRGVDDSTGFRTRNIIICFPFKIKNENQEVIGVAELVNKINGPWFSEKFDSDATA 540
 Db 481 DAYAHPFLFYRGVDDSTGFRTRNIIICFPFKIKNENQEVIGVAELVNKINGPWFSEKFDSDATA 540
 Qy 541 PSYICGSIASHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
 Db 541 PSYICGSIASHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
 Qy 601 FASETYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCIMVKKGYPDPYHNM 660
 Db 601 FASETYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCIMVKKGYPDPYHNM 660
 Qy 661 HAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 720
 Db 661 HAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 720
 Qy 721 SSEGSVMERHHAQAIAILNTHGNCNIFDHFSPKDYQRMMLDMRDIIILATDLAHHLRIFKD 780
 Db 721 SSEGSVMERHHAQAIAILNTHGNCNIFDHFSPKDYQRMMLDMRDIIILATDLAHHLRIFKD 780
 Qy 781 LQKMAEYGYDRTNKHSHLLICLLMTSCDLSDOTKGMKTKIAELIYKEPFSOGDLEKA 840
 Db 781 LQKMAEYGYDRTNKHSHLLICLLMTSCDLSDOTKGMKTKIAELIYKEPFSOGDLEKA 840
 Qy 841 MGNRPMEMDMREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAENREHWTKVS 900
 Db 841 MGNRPMEMDMREKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAENREHWTKVS 900
 Qy 901 HKFTIRGLPSNNSLDFFDEEYVDPDLGAPINGCCSLDAE 942
 Db 901 HKFTIRGLPSNNSLDFFDEEYVDPDLGAPINGCCSLDAE 942
 RESULT 7
 AAY80985
 ID AAY80985 standard; protein; 942 AA.
 XX AC AAY80985;
 XX DT 05-JUN-2000 (first entry)
 XX DE Bovine brain cGS-PDE, SEQ ID NO:43.
 XX KW Phosphodiesterase; calcium; calmodulin; cyclic guanidine monophosphate;
 KW cGMP; cyclic nucleotide; messenger; signal transduction; regulation;
 KW inhibitor; cardiotonic; antidepressant; antihypertensive; antithrombotic.
 XX OS Bos taurus.
 XX XX US6015677-A.
 XX PN 18-JAN-2000.
 XX XX 25-AUG-1998; 98US-00139491.
 XX PF 19-APR-1991; 91US-00688356.
 XX PR 20-APR-1992; 92US-00872644.
 XX PR 29-AUG-1994; 94US-00297494.
 XX PR 31-MAY-1995; 95US-00455525.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Charbonneau H, Sonnenburg WK, Bentley KJ, Beavo JA;
 XX DR WPI; 2000-181142/16.
 XX DR N-PSDB; AAZ90380.
 XX PT Assay for inhibitors of cyclic guanidine monophosphate-stimulated
 PT nucleotide phosphodiesterase, potentially useful as cardiotonic agents.

PT from their ability to alter a heat-shock phenotype.

XX Claim 1; Col 85-90; 69pp; English.

XX The invention relates to purified and isolated nucleotide sequences
CC encoding mammalian Ca²⁺/calmodulin-stimulated phosphodiesterases (CaM-
CC PDEs) and cyclic guanine monophosphate (cGMP)-stimulated
CC phosphodiesterases (cGS-PDEs). In particular the invention relates to an
CC assay for identifying chemicals that modify the enzymatic activity of a
CC mammalian cGS-PDE. The PDEs catalyze the hydrolysis of cyclic
CC nucleotides to their corresponding 5'-nucleoside monophosphates. In this
CC way they control the cellular concentration of cyclic nucleotides,
CC thereby regulating the flow of information from extracellular hormones,
CC neurotransmitters or other signals that use cyclic nucleotides as
CC messengers. The PDEs in turn are regulated by transmembrane signals or
CC second messenger ligands such as Ca²⁺ or cGMP. Inhibitors of these
CC enzymes are potentially useful as cardiotonics, antidiuretics,
CC antihypertensives or antithrombotics. The method of the invention can
CC identify specific inhibitors of particular isoforms of cGS-PDEs.
CC Sequences AAY80968, AAY80972, AAY80975, AAY80984-Y80986, and
CC AAY80988-Y80990 represent isoforms of CaM-PDEs and cGS-PDEs from bovines
CC and humans
XX

SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 3; Length 942;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MCQACGHSILCSQQYPAARPAEPGQQVFLKDEPPPPPCADSLQDALLSLGSVDV	60
DB	1	MCQACGHSILCSQQYPAARPAEPGQQVFLKDEPPPPPCADSLQDALLSLGSVDV	60
QY	61	AGLQAVKALSAVLPKVTVTYLLDGSRLVCEPPELPOEGKRVAVISRRLGNC	120
DB	61	AGLQAVKALSAVLPKVTVTYLLDGSRLVCEPPELPOEGKRVAVISRRLGNC	120
QY	121	GLGPSDLPGKPLARLVAPLAPPTQVLVPLVDKEAGAAVTLVHCGQLSDNEWSLQAV	180
DB	121	GLGPSDLPGKPLARLVAPLAPPTQVLVPLVDKEAGAAVTLVHCGQLSDNEWSLQAV	180
QY	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTQDRKILQCGELYDL	240
DB	181	EKHTLVALKRVQALQORESSVAPEATQNPPEAAGDQGGVAYTQDRKILQCGELYDL	240
QY	241	DASSLQKLVQLQOQETQASRCLLVSDNLQSKVIGDKVLEEEISFPLTTGRGQV	300
DB	241	DASSLQKLVQLQOQETQASRCLLVSDNLQSKVIGDKVLEEEISFPLTTGRGQV	300
QY	301	VEDKKSILQKOLTSQEDMQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360
DB	301	VEDKKSILQKOLTSQEDMQSLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT	360
QY	361	DOEHVIOHCFTYTSVLTSFLAPQEKQLKCEQALQVAKNLFTHLDDVSVLQEIIT	420
DB	361	DOEHVIOHCFTYTSVLTSFLAPQEKQLKCEQALQVAKNLFTHLDDVSVLQEIIT	420
QY	421	EARNLSNAEICSVELLDQNELVAKVFDGGVDESEYIRIPADQGIAGHATTGQILNIP	480
DB	421	EARNLSNAEICSVELLDQNELVAKVFDGGVDESEYIRIPADQGIAGHATTGQILNIP	480
QY	481	DAYAHLPLFYRGVDDSTGFRTRNLCFPIKKNQEVIGVAELVNKINGPWFSDLDATA	540
DB	481	DAYAHLPLFYRGVDDSTGFRTRNLCFPIKKNQEVIGVAELVNKINGPWFSDLDATA	540
QY	541	FSIYCGISIAHSLLYKKVNEAYQRSHLANEMMYHMKVSDDYTKLLHDGIQVPAIDSN	600
DB	541	FSIYCGISIAHSLLYKKVNEAYQRSHLANEMMYHMKVSDDYTKLLHDGIQVPAIDSN	600
QY	601	PASFTYTPRSLPEDDTSMAILSMQDMFNINNYKIDCPTLARFCLMWKGYEDPPYHNW	660
DB	601	PASFTYTPRSLPEDDTSMAILSMQDMFNINNYKIDCPTLARFCLMWKGYEDPPYHNW	660

QY	661	HAFSVSHPCYLLYKXLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFQVASKSVLAALY	720
DB	661	HAFSVSHPCYLLYKXLELTNYLEDMEIPALFISCMCHDLDRGTNNNSFQVASKSVLAALY	720
QY	721	SSEGSVMEHRHFAQAIAIILNTHGCNIFDHFPSKDYORMLDLMDRIILATDLAHLHRIFKD	780
DB	721	SSEGSVMEHRHFAQAIAIILNTHGCNIFDHFPSKDYORMLDLMDRIILATDLAHLHRIFKD	780
QY	781	LQMAEYGVYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA	840
DB	781	LQMAEYGVYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA	840
QY	841	MGNRPMEWMDREKAYIPELQISFMEHIAPIYKLQDLFPKAAELYERVASNREHWTKVS	900
DB	841	MGNRPMEWMDREKAYIPELQISFMEHIAPIYKLQDLFPKAAELYERVASNREHWTKVS	900
QY	901	HKFTIRGLPSSNNSLDFLDEYEVPLDGGARAPINGCCSLDAE	942
DB	901	HKFTIRGLPSSNNSLDFLDEYEVPLDGGARAPINGCCSLDAE	942

RESULT 8

ABUS8724

ID ABUS8724 standard; protein; 942 AA.

XX AC ABUS8724;

XX DT 15-APR-2003 (first entry)

XX DE Bovine brain cGS-PDE.

XX KW Cow; Ca²⁺/calmodulin stimulated phosphodiesterase; enzyme; CaM-PDE;

XX KW 59KDa CaM-PDE; 61KDa CaM-PDE; 63KDa CaM-PDE; cGS-PDE;

XX KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;

XX KW antidiuretic; anti-hypertensive; anti-thrombotic.

XX OS Bos taurus.

XX PN US2002151024-A1.

XX PD 17-OCT-2002.

XX PF 18-JUN-2001; 2001US-00883825.

XX PR 19-APR-1991; 91US-00688356.

XX PR 20-APR-1992; 92US-00872644.

XX PR 31-MAY-1995; 95US-00455526.

XX PR 28-JUL-1998; 98US-00123783.

XX (UNIW) UNIV WASHINGTON.

XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX WPI; 2003-198291/19.

XX N-PSDB; ABX78857.

XX New purified and isolated DNA sequence encoding a mammalian
XX calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide
XX phosphodiesterase polypeptide, useful for therapeutic, diagnostic and
XX prognostic applications.

XX Example 5; Page 46-49; 71pp; English.

XX The invention relates to purified and isolated polynucleotide sequence
XX encoding a mammalian Ca²⁺/calmodulin- or cyclic GMP-stimulated cyclic
XX nucleotide phosphodiesterase polypeptide (CaM-PDE and cGS-PDE). Also
XX included are a DNA vector comprising the novel DNA sequence, a host cell
XX transformed with the polynucleotide sequence, a polypeptide product of
XX the expression in the transformed host cell, an antibody specifically
XX immunoreactive with the polypeptide and assay methods for identifying a
XX chemical agent which modifies the enzymatic activity of a mammalian CaM-
XX PDE or cGS-PDE. Disclosed are the cDNA and protein sequences of bovine
XX 59KDa CaM-PDE, 61KDa CaM-PDE, 63KDa CaM-PDE, cGS-PDE and human 61KDa CaM-

CC PDE and cGS-PDE. The DNA sequence is useful for producing a polypeptide
CC having the enzymatic activity of a mammalian CaM-PDE or cGS-PDE which is
CC used in therapeutic, diagnostic and prognostic applications and in the
CC preparation of antibodies. Isolated chemical agents which are inhibitors
CC of PDEs may have anti-depressant, anti-hypertensive or anti-thrombotic
CC activities or may be cardiotoxic agents. The present sequence is a Bovine
CC CaM-PDE or cGS-PDE (or fragment) of the invention
XX
SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 6; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPPPPPPPCADSLQDALLSLGSDV 60
Db 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPPPPPPPCADSLQDALLSLGSDV 60

Qy 61 AGLOQAVKEALSAVLPKVTETVTVLLDGSRLVCEEPHPELPQEGKREAVISRKLGCN 120
Db 61 AGLOQAVKEALSAVLPKVTETVTVLLDGSRLVCEEPHPELPQEGKREAVISRKLGCN 120

Qy 121 GLGPSDLPGKPLARLVAFLAPDQTVLTVPLVDKAGAAVAVILVHCQGLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQTVLTVPLVDKAGAAVAVILVHCQGLSDNEEWSLQAV 180

Qy 181 EKHTLVALKRVQALQORSSVAPENTQNPPEAAGDQGGVAYTDDRKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQORSSVAPENTQNPPEAAGDQGGVAYTDDRKILQLCGELYDL 240

Qy 241 DASSLQLKVLQYLOQETQASRCCLLVSEDNLQLSCKVIGDKVLEEBISFPLTTRGLQGV 300
Db 241 DASSLQLKVLQYLOQETQASRCCLLVSEDNLQLSCKVIGDKVLEEBISFPLTTRGLQGV 300

Qy 301 VEDKKSILKDLTSEDMOQLQSLMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILKDLTSEDMOQLQSLMGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360

Qy 361 DQDEHVIOHCFHYTSTVLTSIATFOKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIIT 420
Db 361 DQDEHVIOHCFHYTSTVLTSIATFOKEQKLKCEQALLQVAKNLFTHLDDVSVLQELIIT 420

Qy 421 EARLNSNAEICSVFLDQNEILVAKVFDGVDGVEDESYEIRIPADQGIAGHVAATTGQILNIP 480
Db 421 EARLNSNAEICSVFLDQNEILVAKVFDGVDGVEDESYEIRIPADQGIAGHVAATTGQILNIP 480

Qy 481 DAYAHLFYRGVDSGTGFRTRNIIICFPPIKNEHQEVIGVAELVNKINGPWFSEKDEDLATA 540
Db 481 DAYAHLFYRGVDSGTGFRTRNIIICFPPIKNEHQEVIGVAELVNKINGPWFSEKDEDLATA 540

Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGQVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHMKVSDDEYTKLLHDGIGQVAAIDSN 600

Qy 601 FASFTYTPRSIPEDDTSNAIISMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPYNNWM 660
Db 601 FASFTYTPRSIPEDDTSNAIISMLQDMNFINNYKIDCPTLAFCLMVKKGYRDPYNNWM 660

Qy 661 HAFVSVSHFCYLLYKXNLELTNYLEDMEIFALPISCMCHDLDRGTNNFSQVASKSVLAALY 720
Db 661 HAFVSVSHFCYLLYKXNLELTNYLEDMEIFALPISCMCHDLDRGTNNFSQVASKSVLAALY 720

Qy 721 SSEGSMERHHPAQAIATLNTHGNCIFDHFGRKDYQRMMLDMRDIIATDLAHLRIFKD 780
Db 721 SSEGSMERHHPAQAIATLNTHGNCIFDHFGRKDYQRMMLDMRDIIATDLAHLRIFKD 780

Qy 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSQTKGWKTKTKIAELIYKEFFSGDLEKA 840
Db 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSQTKGWKTKTKIAELIYKEFFSGDLEKA 840

Qy 841 MGNRPMEMMDREKAYIPELQISFMEHIAAMPYIKLLQDLFPKAAELYERVAASNRHHTKVS 900
Db 841 MGNRPMEMMDREKAYIPELQISFMEHIAAMPYIKLLQDLFPKAAELYERVAASNRHHTKVS 900

Qy 301 HKFTIRGLPSNNSLDFDEEYVDPDLGARAPINGCCSLDAE 942
Db 301 HKFTIRGLPSNNSLDFDEEYVDPDLGARAPINGCCSLDAE 942

RESULT 9

ADQ94963

ID ADQ94963 standard; protein; 942 AA.

AC ADQ94963;

DT 23-SEP-2004 (first entry)

XX Bovine cGS-PDE protein, pBBCGSPDE-7.

DE CaM-PDE;

KW Ca 2+/ calmodulin stimulated cyclic nucleotide phosphodiesterase; cGMP;

KW cyclic-guanosine monophosphate; cGS-PDE;

KW cyclic-GMP stimulated cyclic nucleotide phosphodiesterase; bovine.

OS Bos sp.

XX US2004126866-A1.

FN 01-JUL-2004.

PD 30-OCT-2003; 2003US-00697894.

XX 19-APR-1991; 91US-00688356.

XX 20-APR-1992; 92US-00872644.

PR 29-AUG-1994; 94US-00297494.

PR 31-MAY-1995; 95US-00455526.

PR 28-JUL-1998; 98US-00123783.

PR 18-JUN-2001; 2001US-00883825.

XX (BEAV/) BEAVO J A.

PA (BENT/) BENTLEY J K.

PA (CHAR/) CHARBONNEAU H.

PA (SONN/) SONNENBURG W K.

PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX WPI; 2004-516912/49.

DR N-PSDB; ADQ94962.

XX Novel mammalian calcium/calmodulin stimulated cyclic phosphodiesterase

PT nucleotide sequence useful for identifying chemical agent that modifies

PT enzymatic activity of calcium/calmodulin stimulated cyclic

PT phosphodiesterase polypeptide.

XX Example 5; SEQ ID NO 43; 72pp; English.

PS The present invention provides a mammalian Ca 2+/ calmodulin stimulated

XX cyclic nucleotide phosphodiesterase (CaM-PDE) and cyclic-guanosine

CC monophosphate (cGMP) stimulated cyclic nucleotide phosphodiesterase (cGS-

CC PDE) polypeptide and its polynucleotide. The invention is useful for

CC producing a polypeptide having enzymatic activity of mammalian CaM-PDE

CC and cGS-PDE. The invention is also useful for identifying a chemical

CC agent that modifies the enzymatic activity of mammalian CaM-PDE and cGS-

CC PDE. The present sequence is bovine cGS-PDE protein, pBBCGSPDE-7.

XX SQ Sequence 942 AA;

Query Match 100.0%; Score 4911; DB 8; Length 942;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPPPPPPPCADSLQDALLSLGSDV 60

Db 1 MGQACGSHILCRSQYPAARPAERPGQVFLKPDPPPPPPPCADSLQDALLSLGSDV 60

Qy 61 AGLOQAVKEALSAVLPKVTETVTVLLDGSRLVCEEPHPELPQEGKREAVISRKLGCN 120

Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKVRNAVSRKRLGNC 120
Qy 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAVILVHCQGLSDNEESLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAVILVHCQGLSDNEESLQAV 180
Qy 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEBAAGDQKGGVAYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEBAAGDQKGGVAYTDQDRKILQCGELYDL 240
Qy 241 DASSLQLKVLQVLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300
Db 241 DASSLQLKVLQVLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300
Qy 301 VEDKKSILQKDLTSEDMDQGLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSEDMDQGLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 360
Qy 361 DQDEHVIQCHFYTSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
Db 361 DQDEHVIQCHFYTSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
Qy 481 DAYAHLPLVRGVDDSTGFRNLICFPPIKNEQVIGVAVELVKNKINGPWFSPFDEDLATA 540
Db 481 DAYAHLPLVRGVDDSTGFRNLICFPPIKNEQVIGVAVELVKNKINGPWFSPFDEDLATA 540
Qy 541 FSIYCGISIAHLLYKKNVNEAQRSHLANEMMYHMKVSDDEYTKLLHDGIIQFVAADSN 600
Db 541 FSIYCGISIAHLLYKKNVNEAQRSHLANEMMYHMKVSDDEYTKLLHDGIIQFVAADSN 600
Qy 601 FASFTYTPRSLPDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKGYRDPHYHNM 660
Db 601 FASFTYTPRSLPDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKGYRDPHYHNM 660
Qy 661 HAFSVSHFCYLYKNLELTNYLEDMEIPALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 720
Db 661 HAFSVSHFCYLYKNLELTNYLEDMEIPALFTSCMCHDLDRGTNNNSFOVASKSVLAALY 720
Qy 721 SSEGSVMERHHPAQAIILNTHGNCIFDHFSRKYQRMFLMRDILATDLAHLRIKFD 780
Db 721 SSEGSVMERHHPAQAIILNTHGNCIFDHFSRKYQRMFLMRDILATDLAHLRIKFD 780
Qy 781 LQKMAEVGYDRTNKQHSLLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFPFSGDLEKA 840
Db 781 LQKMAEVGYDRTNKQHSLLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFPFSGDLEKA 840
Qy 841 MGNRPWEMMDREKAYIPELQISFMHIAMPIYKLLQDLPPKAAELYERVASNRHHTKVS 900
Db 841 MGNRPWEMMDREKAYIPELQISFMHIAMPIYKLLQDLPPKAAELYERVASNRHHTKVS 900
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSIDAE 942
Db 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSIDAE 942

RESULT 10
AAR28408
ID AAR28408 standard; protein; 942 AA.
XX
AC AAR28408;
XX
XX
DT 25-MAR-2003 (revised)
DT 19-MAR-1993 (first entry)
XX
DE CGS PDE from bovine brain clone pBBCGSPDE-7.
XX
KW Cyclic GMP; stimulated; cyclic; nucleotide; bovine brain;
KW phosphodiesterase; hybridisation; ss.

XX OS Bos taurus.
XX PN W09218541-A1.
XX PD 29-OCT-1992.
XX PF 20-APR-1992; 92WO-US0003222.
XX PR 19-APR-1991; 91US-00688356.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
XX DR WPI; 1992-382051/46.
XX DR N-PSDB; AAQ30183.
XX PT New DNA encoding mammalian cyclic nucleotide phospho-di:esterase - and
XX PT derived vectors and host cells, useful for screening cpds. for inhibitory
XX PT or activating activity.
XX PS Example 5B; Page 91; 133pp; English.
XX CC A bovine brain cDNA library in lambda ZAP was screened with a 450 bp
XX CC Scori/apai fragment of p3CGS-5 cDNA corresp. to p3CGS-5 nucleotide
XX CC position numbers 1-452. Forty putative clones were picked from this first
XX CC screen, of which six were randomly selected and purified. Each of the
XX CC clones was spotted onto a lawn of host X11 cells and screened with a 370
XX CC bp PstI/SmaI fragment of p3CGS-5 cDNA. Six putative clones were obt'd. and
XX CC sequenced. Clone pBBCGSPDE-7 contains an insert contg. an ORF encoding a
XX CC 942 residue protein that is nearly identical to the adrenal gland CGS-PDE
XX CC isozyme. The difference in the primary structure of these two isozymes
XX CC lies in the amino terminal residues 1-46 of the brain CGS PDE and
XX CC residues 1-25 of the adrenal CGS PDE. The remaining carboxy-terminal
XX CC residues of the brain and adrenal CGS PDE are identical. (Updated on 25-
XX CC MAR-2003 to correct PN field.)
XX SQ Sequence 942 AA;

Query Match 99.2%; Score 4871; DB 2; Length 942;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 934; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MQACGCHILCRSQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDV 60
Db 1 MQACGCHILCRSQYPAARPAEPGRGQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDV 60
Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKVRNAVSRKRLGNC 120
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKVRNAVSRKRLGNC 120
Qy 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAVILVHCQGLSDNEESLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDQVLVPLVDKEAGAAVAVILVHCQGLSDNEESLQAV 180
Qy 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEBAAGDQKGGVAYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPEATQNPPEBAAGDQKGGVAYTDQDRKILQCGELYDL 240
Qy 241 DASSLQLKVLQVLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300
Db 241 DASSLQLKVLQVLOQETOASRCLLLVSEDNLQSKVIGDKVLEEEISFPFLLTGRGQV 300
Qy 301 VEDKKSILQKDLTSEDMDQGLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSEDMDQGLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 360
Qy 361 DQDEHVIQCHFYTSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
Db 361 DQDEHVIQCHFYTSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480


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Db      840 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 899
Qy      901 HKFTIRGLPSNNSLDFLDEEYEPDLDGARAPINGCCSLDAE 942
Db      900 HKFTIRGLPSNNSLDFLDEEYEPDLDGTRAPINGCCSLDAE 941

RESULT 12
AAW11253
ID AAW11253 standard; protein; 941 AA.
XX
AC AAW11253;
XX
DT 25-MAR-2003 (revised)
DT 17-MAR-1997 (first entry)
XX
DE pHCgs6n cyclic GMP stimulated phosphodiesterase.
XX
KW Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP;
KW adrenal gland; cGMP; transmembrane signal; extracellular hormone;
KW neurotransmitter; antibody; human.
XX
OS Homo sapiens.
XX
PN US5580771-A.
XX
PD 03-DEC-1996.
XX
PF 29-AUG-1994; 94US-00297494.
XX
PR 19-APR-1991; 91US-00688356.
XX
PR 20-APR-1992; 92US-00872644.
XX
PA (UNITW ) UNIV WASHINGTON.
XX
PI Charbonneau H, Sonnenburg WK, Beavo JA;
XX
WPI; 1997-033573/03.
DR N-PSDB; AAT51113.
XX
DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
recombinant enzyme.
XX
Example 6; Col 89-96; 68pp; English.
XX
CC This sequence represents the cyclic GMP stimulated phosphodiesterase (cGS
CC -PDE) clone pHCgs6n isolated from human foetal brain. The cyclic
CC nucleotide phosphodiesterases (PDEs) catalyse the hydrolysis of 3', 5'
CC cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'-
CC nucleotide monophosphates. The PDEs are therefore important in the
CC control of the cellular concentration of cyclic nucleotides. The PDEs
CC are, in turn, regulated by transmembrane signals or second messenger
CC ligands such as calcium ion or cGMP. The PDEs therefore have a central
CC role in regulating the flow of information from extracellular hormones,
CC neurotransmitters, or other signals that use the cyclic nucleotides as
CC messengers. PDEs are present in most of the cells and tissues of
CC eukaryotic organisms, but only in trace amounts. cGS-PDEs are stimulated
CC by cGMP in effecting cAMP hydrolysis. This is thought to occur through a
CC noncatalytic cGMP-specific site present on the cGS-PDE. The cDNA encoding
CC this sequence can be used for the production of recombinant cGS-PDE,
CC which may have therapeutic and diagnostic uses. This protein may also be
CC useful for diagnostic antibody production. (Updated on 25-MAR-2003 to
CC correct PF field.)
XX
SQ Sequence 941 AA;
Query Match 96.3%; Score 4728.5; DB 2; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatch 19; Indels 1; Gaps 1;
Qy      1 MQQACGSHILCSQQYPAARPAEPRGQQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDV 60
|||||
1 MQQACGSHILCSQQYPAARPAEPRGQQVFLKPDPPPPPPQPCADSLQDALLSLGSVIDI 60
61 AGLOQAVKEALSAVLPKIVETVYTYLLDGSERLVCEBPPHQLPQEGKREAVISRKLGCN 120
|||||
61 SGLQRAVKEALSAVLPKIVETVYTYLLDGSERLVCEBPPHQLPQEGKREAVISRKLGCN 120
|||||
121 GLGPSDLFGKPLARLVAFLAPDTQVLPVDKEAGAVAAVILVHCGQLSDNEEWSLQAV 180
|||||
121 GLGPSDLFGKPLARLVAFLAPDTQVLPVDKEAGAVAAVILVHCGQLSDNEEWSLQAV 180
|||||
181 EKHTLVALKRVQALQORESSVAPEATONPPBEAAGDQGGVAYTQDRLKILQCGELYDL 240
|||||
181 EKHTLVALKRVQALQORESSVAPEATONPPBEAAGDQGGVAYTQDRLKILQCGELYDL 240
|||||
241 DASSLQKLVLOYLQOETQASRCCLLVSEDNLQLSCKVIGDKVLBEEISFPFLLTGRGV 300
|||||
241 DASSLQKLVLOYLQOETQASRCCLLVSEDNLQLSCKVIGDKVLBEEISFPFLLTGRGV 300
|||||
301 VEDKKSIOIKDLTSEDMOQLQSMGLCEVQMLCVPIVSRATQVVALACAFNKLGGDLFT 360
|||||
300 VEDKKSIOIKDLTSEDVQQLQSMGLCEVQMLCVPIVSRATQVVALACAFNKLGGDLFT 359
|||||
361 DQDEHVIQHCFTYTTSTLTSTLAFQKQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420
|||||
360 DQDEHVIQHCFTYTTSTLTSTLAFQKQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 419
|||||
421 EARNLSNAEICSVFLLDQNELVAKVFDGVDSEYEIRIPADQGIAGHVAITGQILNIP 480
|||||
420 EARNLSNAEICSVFLLDQNELVAKVFDGVDSEYEIRIPADQGIAGHVAITGQILNIP 479
|||||
481 DAYAHLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVAELVNKINGPWFSPFDEDLATA 540
|||||
480 DAYAHLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVAELVNKINGPWFSPFDEDLATA 539
|||||
541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSN 600
|||||
540 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIPVAAIDSN 599
|||||
601 FASFTYTPRSIPEDDTSMALLSMLQDMNFNNYKIDCPTLAFCLMVKKGYRDPYPHNNW 660
|||||
600 FASFTYTPRSIPEDDTSMALLSMLQDMNFNNYKIDCPTLAFCLMVKKGYRDPYPHNNW 659
|||||
661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRHGTNNNSFOVASKSVLAALY 720
|||||
660 HAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLDRHGTNNNSFOVASKSVLAALY 719
|||||
721 SSEGSMERHHPAQAIATLNTHGCHI FDHFSRKYORMDLMDRDIILATDLAHLRIFKD 780
|||||
720 SSEGSMERHHPAQAIATLNTHGCHI FDHFSRKYORMDLMDRDIILATDLAHLRIFKD 779
|||||
781 LQKMAEVGYDRTNKOHSLLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
|||||
780 LQKMAEVGYDRNNKQHRLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 839
|||||
841 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
|||||
840 MGNRPMMMDREKAYIPQLQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 899
|||||
901 HKFTIRGLPSNNSLDFLDEEYEPDLDGARAPINGCCSLDAE 942
|||||
900 HKFTIRGLPSNNSLDFLDEEYEPDLDGTRAPINGCCSLDAE 941
|||||

RESULT 13
AAW18050
ID AAW18050 standard; protein; 941 AA.
XX
AC AAW18050;
XX
DT 25-MAR-2003 (revised)
DT 05-AUG-1997 (first entry)
XX
DE Human cGS-PDE amino acid sequence from pHCgs6n.
```


XX Cyclic-GMP-stimulated phosphodiesterase; antibody; human;
KW polymerase chain reaction.
XX Homo sapiens.
XX US5602019-A.
XX PD 11-FEB-1997.
XX PF 29-AUG-1994; 94US-00297510.
XX PR 19-APR-1991; 91US-00688356.
XX PR 20-APR-1992; 92US-00872644.
XX (UNIW) UNIV WASHINGTON.
XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;
XX WPI; 1997-131799/12.
XX DR N-PSDB; AAT67224.
XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated by
XX calcium/calmodulin, useful for recombinant prodn. of the enzymes.
XX Example 6; Col 97-102; 69pp; English.
XX The present sequence represents the human cyclic-GMP-stimulated
XX phosphodiesterase (cGS-PDE) from pHCs6n plasmid. The DNA sequences of
XX the cGS-PDE's are used for the production of the recombinant enzymes,
XX which in turn may be used for antibody production and to screen for
XX compounds that modulate phosphodiesterase activity. (Updated on 25-MAR-
XX 2003 to correct Pf field.) (Updated on 25-MAR-2003 to correct Pf field.)
XX SQ Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGSHILCRSQQYPAARPAEPGRQGVFLKPDPEPPPPQPCADSLQDALLSLGSDVD 60
Db 1 MGQACGSHILCRSQQYPAARPAEPGRQGVFLKPDPEPPPPQPCADSLQDALLSLGSDVD 60
QY 61 AGLQAVKEALSAVLPRVETVYTYLLDGSRLVCEPPELPOEGKVREAVISQKRLGCN 120
Db 61 SGLQRAVKEALSAVLPRVETVYTYLLDGSRLVCEPPELPOEGKVREAVISQKRLGCN 120
QY 121 GLGFSDLPGKPLARLAVPLADPTQVLVPLVDKAGAAVAVILVHCGQLSDNEWSLQAV 180
Db 121 GLGFSDLPGKPLARLAVPLADPTQVLVPLVDKAGAAVAVILVHCGQLSDNEWSLQAV 180
QY 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDQKGVAYTDDRKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDQKGVAYTDDRKILQLCGELYDL 240
QY 241 DASSLQLKVLQVLOQETQASRCLLLVSEDNLQLSCKVIGKVLBEESFPILTTGRIGQV 300
Db 241 DASSLQLKVLQVLOQETQASRCLLLVSEDNLQLSCKVIGKVLBEESFPILTTGRIGQV 300
QY 301 VEDKKSICQLDLSDEMOQLSMLGCEVOAMLCPVVISRATDQVVALACAFNKLGGDLFT 360
Db 300 VEDKKSICQLDLSDEMOQLSMLGCEVOAMLCPVVISRATDQVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQCHFYTSVLTSTLAFQEKQKJCEQALLQVAKNLFTHLDDSVLLQEIIIT 420
Db 360 DQDEHVIQCHFYTSVLTSTLAFQEKQKJCEQALLQVAKNLFTHLDDSVLLQEIIIT 420
QY 421 EARNLSNAEISCVFLLDQNELVAKVFDGCVVEDESYEIRIPADQIAGHVATTGQILNIP 480
Db 420 EARNLSNAEISCVFLLDQNELVAKVFDGCVVEDESYEIRIPADQIAGHVATTGQILNIP 480
QY 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFPSKFDSDATA 540

Db 480 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQVIGVAELVNKINGPWFPSKFDSDATA 539
QY 541 PSYICGSIASHSLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
Db 540 PSYICGSIASHSLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 599
QY 601 PASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNM 660
Db 600 PASFTYTPRSIPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCIMVKKGVRDPPYHNM 659
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALY 720
Db 660 HAFSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLDRGTNNNSFQVASKSVLAALY 719
QY 721 SSEGSMERHHAQAIAILNTHGNCIFDHFPSRKDYQRMQLDMRDIIILATDLAHLURIFKD 780
Db 720 SSEGSMERHHAQAIAILNTHGNCIFDHFPSRKDYQRMQLDMRDIIILATDLAHLURIFKD 779
QY 781 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSDOTKGMKTKTKIAELIYKEFPFSGDLEKA 840
Db 780 LQKMAEYGYDRTNKHSHLLCLLMTSCDLSDOTKGMKTKTKIAELIYKEFPFSGDLEKA 839
QY 841 MGNRPMEWMDEKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAENREHWTKVS 900
Db 840 MGNRPMEWMDEKAYIPELQISFMEHIAMPYIKLLQDLFPKAAELYERVAENREHWTKVS 899
QY 901 HKFTIRGLPSNNSLDLDEEYVDPDLOGARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDLDEEYVDPDLOGARAPINGCCSLDAE 941

RESULT 14
AAW71226
ID AAW71226 standard; protein; 941 AA.
XX AC AAW71226;
XX DT 29-OCT-1998 (first entry)
XX DE Human cGS-PDE cDNA protein sequence.
XX KW Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; Cam-PDE;
XX KW assay; identification; modification; enzymatic activity; modulator;
XX KW cyclic guanosine monophosphate-stimulated phosphodiesterase; cGS-PDE;
XX KW human.
XX OS Homo sapiens.
XX PN US5800987-A.
XX PD 01-SEP-1998.
XX PF 31-MAY-1995; 95US-00455525.
XX PR 19-APR-1991; 91US-00688356.
XX PR 20-APR-1992; 92US-00872644.
XX PR 29-AUG-1994; 94US-00297494.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;
XX DR WPI; 1998-494762/42.
XX DR N-PSDB; AAV54762.
XX PT Identification of modulators of Calcium/calmodulin sensitive cyclic
XX PT nucleotide phosphodiesterase - uses recombinant cells expressing the
XX PT enzyme and monitoring protein expression in the presence of potential
XX PT modulators.
XX PS Example 6; Col 97-102; 69pp; English.
XX

CC The present sequence represents human cyclic guanosine monophosphate-
CC stimulated phosphodiesterase (cG5-PDE) cDNA. The specification also
CC describes Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase
CC (Cam-PDE) enzymes. Cam-PDE enzymes catalyze the hydrolysis of cyclic
CC nucleotides and as such control their intracellular level. They are
CC controlled by second messengers e.g. Ca2+ and calmodulin and
CC transmembrane signals and through pathways involving these, regulate flow
CC of information from extracellular hormones, neurotransmitters and other
CC signals using cyclic nucleotides as messengers. The specification
CC describes an assay for identifying a chemical agent which modifies the
CC enzymatic activity of a mammalian Cam-PDE. The assays are useful for
CC identifying modulators of Cam-PDEs. The assay is carried out by
CC incubating cells expressing Cam-PDE with the suspected modulator and
CC measuring its effect e.g. monitoring the hydrolysis of cAMP and/or cGMP
XX Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQQACGHSILCRSQQYPAARPAERPGQVFLKDEPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MQQACGHSILCRSQQYPAARPAERPGQVFLKDEPPPPPPQCADSLQDALLSLGSDIV 60

Qy 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHELPOEGKREAVISRKLGCN 120
Db 61 SGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHELPOEGKREAVISRKLGCN 120

Qy 121 GLGPDPLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEVSQAV 180
Db 121 GLGPDPLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEVSQAV 180

Qy 181 EKHTLVALKRVQALQORESSVAPEATONPPEAAGDKGGVAYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATONPPEAAGDKGGVAYTDQDRKILQCGELYDL 240

Qy 241 DASSLQLKVLQYLOQETQASRCCLLLVSDNQLQSKCKVIGDKVLEEEISFPITTRGLQV 300
Db 241 DASSLQLKVLQYLOQETQASRCCLLLVSDNQLQSKCKVIGDKVLEEEISFPITTRGLQV 300

Qy 301 VEDKKSILQKLTSDMQQLQSMQCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360
Db 301 VEDKKSILQKLTSDMQQLQSMQCEVQAMLCVPVISRATDQVVALACAFNKGDLFT 360

Qy 361 DQDEHVIQCHFYTSTLTSTLAFQKQKCECQALLQVAKNLFTHLDDVSVLLQETIT 420
Db 361 DQDEHVIQCHFYTSTLTSTLAFQKQKCECQALLQVAKNLFTHLDDVSVLLQETIT 420

Qy 421 EARLNSNAEICSVFLLDQNELVAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIP 480
Db 421 EARLNSNAEICSVFLLDQNELVAKVFDGGVDESEYRIPADQGIAGHVATTGQILNIP 480

Qy 481 DAYAHLFVRGDDSTGFRTRNLCPFKIKNQEVIGVVAELVKNKINGPMWFKFDBDLATA 540
Db 481 DAYAHLFVRGDDSTGFRTRNLCPFKIKNQEVIGVVAELVKNKINGPMWFKFDBDLATA 540

Qy 541 PSYICGSIASHSLYKKNQYRSHLANEMMYHMKVSDDEYTKLHDGTPVAAIDSN 600
Db 541 PSYICGSIASHSLYKKNQYRSHLANEMMYHMKVSDDEYTKLHDGTPVAAIDSN 600

Qy 601 PASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNMW 660
Db 601 PASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMWKGYRDPYHNMW 660

Qy 661 HAFVSVHFCYLLYKNLENTYLEDMEIFALFISCMCHDLDRGTNNSQVASKSVLAALY 720
Db 661 HAFVSVHFCYLLYKNLENTYLEDMEIFALFISCMCHDLDRGTNNSQVASKSVLAALY 720

Qy 721 SSEGVSWEHRHFAQAIALNTHGNCIFDHFSRKDYQRMQLDMLRDIIATDLAHLRIFKD 780
Db 721 SSEGVSWEHRHFAQAIALNTHGNCIFDHFSRKDYQRMQLDMLRDIIATDLAHLRIFKD 780

Qy 779 SSEGVSWEHRHFAQAIALNTHGNCIFDHFSRKDYQRMQLDMLRDIIATDLAHLRIFKD 779
Db 779 SSEGVSWEHRHFAQAIALNTHGNCIFDHFSRKDYQRMQLDMLRDIIATDLAHLRIFKD 779

Qy 781 LQMAEVGYDRTNKKOHHSLLCLLMTSCDLSQTKGWTKTKRIAEIYKEPFSQGDLEKA 840
Db 780 LQMAEVGYDRTNKKOHHSLLCLLMTSCDLSQTKGWTKTKRIAEIYKEPFSQGDLEKA 839

Qy 841 MGNRPMEWMMDREKAYIPELOISFMEHIAMPIYKQLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMEWMMDREKAYIPELOISFMEHIAMPIYKQLQDLFPKAAELYERVASNRHWTKVS 899

Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGGARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVPLDGGARAPINGCCSLDAE 941

RESULT 15
AAW77042
ID AAW77042 standard; protein; 941 AA.
XX AC AAW77042;
XX DT 14-DEC-1998 (first entry)
XX DE Cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n.
XX KW cow; Ca2+ stimulated phosphodiesterase;
XX KW Calmodulin stimulated phosphodiesterase; therapeutic; antibody.
XX OS Bos sp. -
XX PN US5789553-A.
XX PD 04-AUG-1998.
XX PF 31-MAY-1995; 95US-00455526.
XX PR 19-APR-1991; 91US-00688356.
XX PR 20-APR-1992; 92US-00872644.
XX PR 29-AUG-1994; 94US-00297494.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Sonnenburg WK, Charbonneau H, Beavo JA, Bentley JK;
XX WPI; 1998-446185/38.
XX DR N-PSDB; AAV48205.
XX PT Antibody to phosphodiesterase polypeptide - useful for purification or
XX PT detection of polypeptide.
XX PS Example 6; Column 89/96; 68pp; English.
XX CC The cyclic-GMP-stimulated phosphodiesterase clone pHcgs6n encodes a
XX CC phosphodiesterase from the bovine brain. The phosphodiesterases isolated
XX CC in this invention were used to transform host cells, preferably mammalian
XX CC or yeast cells. The recombinant proteins and fragments produced can be
XX CC used for therapeutic, diagnostic, and prognostic purposes and will
XX CC provide the basis for preparation of monoclonal and polyclonal
XX CC antibodies. An antibody specific for the Ca2+/calmodulin-stimulated
XX CC cyclic nucleotide phosphodiesterase (PDE) polypeptide is useful for
XX CC affinity purification or detection of the polypeptide and is selective
XX CC only for the Ca2+/calmodulin stimulated cyclic nucleotide PDE polypeptide
XX SQ Sequence 941 AA;

Query Match 96.3%; Score 4728.5; DB 2; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQQACGHSILCRSQQYPAARPAERPGQVFLKDEPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MQQACGHSILCRSQQYPAARPAERPGQVFLKDEPPPPPPQCADSLQDALLSLGSDIV 60

Qy 61 AGLOQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHELPOEGKREAVISRKLGCN 120
Db 61 SGLQAVKEALSAVLPKVETVYTYLLDGSRLVCEPPHELPOEGKREAVISRKLGCN 120

Db 61 SGLQRAVKEALSAVLPRVETVYTYLLDGSQVLCBDDPPHELQEGKVREAIISQKRLGCN 120
Qy 121 GLGPSDLQKPLARLAVAPLADPTQVTVIPLVDKEAGAAVAVTLVHCGQISDNEEWSLOAV 180
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Db 300 VEDKXSIQIKDLTSDMQLOSLMGLCEVOAMLCVPIVSRATDQVVALACAFNKLGGDLFT 360
Qy 361 DODEHVIQCHFYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLLOEIIIT 420
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Qy 421 EARNLSNAEICSFVLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 480
Db 420 EARNLSNAEICSFVLLDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTGQILNIP 479
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVLAELVKNKINGPWFKFDLATA 540
Db 480 DAYAHLPLFYRGVDDSTGFRTRNILCFPIKNENQEVIGVLAELVKNKINGPWFKFDLATA 539
Qy 541 FSIYCGISIAHSLLYKKNQYRSHLANEMMMYHMKVSDDBEYTKLLHDGIQPVAAIDSN 600
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Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMWKKGYRDPYPYHNM 660
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Qy 661 HAFVSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLHRGTNNSFOVASKSVLAALY 720
Db 660 HAFVSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLHRGTNNSFOVASKSVLAALY 719
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Db 720 SSEGSVMERHHPAQAIATLNTHGNCIPDHFSKDYORMLDLMDRIILATDLAHLRIPKD 779
Qy 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 839
Qy 841 MGNRPMENMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMENMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDLDEEVEVDPDLDGARAPINGCCSLDAE 942
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OM protein - protein search, using sw model

Run on: June 26, 2005, 12:10:37 ; Search time 30.8438 Seconds
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Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4911	100.0	942	1 US-07-872-644-43	Sequence 43, Appl
2	4911	100.0	942	1 US-08-297-494-43	Sequence 43, Appl
3	4911	100.0	942	1 US-08-297-510-43	Sequence 43, Appl
4	4911	100.0	942	1 US-08-479-532-43	Sequence 43, Appl
5	4911	100.0	942	1 US-08-455-525-43	Sequence 43, Appl
6	4911	100.0	942	1 US-08-455-525-43	Sequence 43, Appl
7	4911	100.0	942	3 US-09-139-491-43	Sequence 43, Appl
8	4911	100.0	942	4 US-09-883-825-43	Sequence 43, Appl
9	4911	100.0	942	5 PCT-US92-03222-43	Sequence 43, Appl
10	4728.5	96.3	941	1 US-07-872-644-45	Sequence 45, Appl
11	4728.5	96.3	941	1 US-08-297-494-45	Sequence 45, Appl
12	4728.5	96.3	941	1 US-08-297-510-45	Sequence 45, Appl
13	4728.5	96.3	941	1 US-08-479-532-45	Sequence 45, Appl
14	4728.5	96.3	941	1 US-08-455-525-45	Sequence 45, Appl
15	4728.5	96.3	941	1 US-08-455-525-45	Sequence 45, Appl
16	4728.5	96.3	941	3 US-09-139-491-45	Sequence 45, Appl
17	4728.5	96.3	941	4 US-09-883-825-45	Sequence 45, Appl
18	4728.5	96.3	941	4 US-09-708-392-5	Sequence 5, Appl
19	4728.5	96.3	941	4 US-09-949-016-6244	Sequence 6244, Ap
20	4728.5	96.3	941	5 PCT-US92-03222-45	Sequence 45, Appl
21	4657	94.8	921	1 US-07-872-644-39	Sequence 39, Appl
22	4657	94.8	921	1 US-08-297-494-39	Sequence 39, Appl
23	4657	94.8	921	1 US-08-297-510-39	Sequence 39, Appl
24	4657	94.8	921	1 US-08-479-532-39	Sequence 39, Appl
25	4657	94.8	921	1 US-08-455-525-39	Sequence 39, Appl
26	4657	94.8	921	1 US-08-455-525-39	Sequence 39, Appl
27	4657	94.8	921	3 US-09-139-491-39	Sequence 39, Appl

28	4657	94.8	921	3 US-09-754-250-5	Sequence 5, Appl
29	4657	94.8	921	4 PCT-US92-03222-39	Sequence 39, Appl
30	4657	94.8	921	5 US-09-754-250-4	Sequence 39, Appl
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33	3815	77.7	802	4 US-09-949-016-7922	Sequence 7922, Ap
34	913.5	18.6	779	2 US-08-951-648-6	Sequence 6, Appl
35	913.5	18.6	779	3 US-09-174-437-6	Sequence 6, Appl
36	913.5	18.6	779	4 US-09-686-055A-6	Sequence 1, Appl
37	913.5	18.6	779	4 US-09-420-190-1	Sequence 1, Appl
38	912	18.6	803	2 US-08-951-648-4	Sequence 4, Appl
39	912	18.6	803	3 US-09-174-437-4	Sequence 4, Appl
40	912	18.6	803	4 US-09-686-055A-4	Sequence 4, Appl
41	911.5	18.6	766	2 US-08-951-648-2	Sequence 2, Appl
42	911.5	18.6	766	3 US-09-174-437-2	Sequence 2, Appl
43	911.5	18.6	766	4 US-09-686-055A-2	Sequence 2, Appl
44	804	16.4	875	1 US-08-480-547A-23	Sequence 23, Appl
45	804	16.4	875	1 US-08-250-847B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-07-872-644-43
; Sequence 43, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSES: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-43

Query Match 100.0% Score 4911; DB 1; Length 942;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 181 EKHTLVALKRVQALQORRESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL 240

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Db 241 DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV 300

Qy 301 VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
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RESULT 2

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US-08-297-494-43
; Sequence 43, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
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; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5580771and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-297-494-43
```

```
Query Match 100.0%; Score 4911; DB 1; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQACGHSILCRSQYPAARPAERPGQQVFLKPDPEPPPPPCADSLQDALLSLGSDVDV 60
Db 1 MGQACGHSILCRSQYPAARPAERPGQQVFLKPDPEPPPPPCADSLQDALLSLGSDVDV 60

Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPELHPQEGKREAVISRKLGCN 120
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPELHPQEGKREAVISRKLGCN 120

Qy 121 GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180
Db 121 GLGPSDLPGKPLARLAPLAPDQVLPVLDKEAGAAVAVILVHCGQLSDNEEWSLOAV 180

Qy 181 EKHTLVALKRVQALQORRESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQORRESSVAPEATQNPPEAAGDQGGVAYTDQDRKILQCGELYDL 240

Qy 241 DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV 300
Db 241 DASSLQKLVQLQOETQASRCCLLVSEDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV 300

Qy 301 VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSEDMDQQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360

Qy 361 DQDEHVIQHCFTYTSVLTSTLAFQEKQKCECOALLQVAKNLFTHLDDVSVLLQEIT 420
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Db 361 DQEHVIOHCFHYTSTVLTSTLAFOKEQKKECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVEIGVAELVKNKINGPWFSPKDEDELATA 540
Db 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVEIGVAELVKNKINGPWFSPKDEDELATA 540
QY 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDCIOPVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDCIOPVAAIDSN 600
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVYHNM 660
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVYHNM 660
QY 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Db 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
QY 721 SSEGSMERHHPAQAIATILNTHGNCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD 780
Db 721 SSEGSMERHHPAQAIATILNTHGNCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD 780
QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLK 840
Db 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLK 840
QY 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
Db 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
QY 901 HKFTIRGLPNSNLSDFLDEYEVPLDGGARAPINGCCSLDAE 942
Db 901 HKFTIRGLPNSNLSDFLDEYEVPLDGGARAPINGCCSLDAE 942

RESULT 3

US-08-297-510-43
; Sequence 43, Application US/08297510
; Patent No. 5602019
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSES: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991

; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-297-510-43

Query Match 100.0%; Score 4911; DB 1; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQQACGHSILCRSQYPAARPAERGGQVFLKPDDEPPPPQPCADSLQDALLSLGSDIV 60
Db 1 MQQACGHSILCRSQYPAARPAERGGQVFLKPDDEPPPPQPCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHLPQEGKVRKAVISRKLGCN 120
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHLPQEGKVRKAVISRKLGCN 120
QY 121 GIGPSDLCPKLARLAVPLAPDTQVILVPLVDKEAGAAVILVHCGQLSDNEEWSLQAV 180
Db 121 GIGPSDLCPKLARLAVPLAPDTQVILVPLVDKEAGAAVILVHCGQLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVQALQRESSVAPEATQNPPEEAAGQKGVAYTQDQRKILQICGELYDL 240
Db 181 EKHTLVALKRVQALQRESSVAPEATQNPPEEAAGQKGVAYTQDQRKILQICGELYDL 240
QY 241 DASSILQLKVLQVLOQETOASRCCLLVSEDNIQLSKVJGDKVLEBEISFPLTTGRGQV 300
Db 241 DASSILQLKVLQVLOQETOASRCCLLVSEDNIQLSKVJGDKVLEBEISFPLTTGRGQV 300
QY 301 VEDKESIQLKDLTSEDMOQLQSMGCEVOAMLCPVISRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKESIQLKDLTSEDMOQLQSMGCEVOAMLCPVISRATQVVALACAFNKLGGDLFT 360
QY 361 DQEHVIOHCFHYTSTVLTSTLAFOKEQKKECQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQEHVIOHCFHYTSTVLTSTLAFOKEQKKECQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABICSVFLDDQNELVAKVFDGGVDESEYIIRIPADQGIAGHVATTGQILNIP 480
QY 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVEIGVAELVKNKINGPWFSPKDEDELATA 540
Db 481 DAYAHLPLFYRGVDDSTGFRTRNLCFPIKNEQVEIGVAELVKNKINGPWFSPKDEDELATA 540
QY 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDCIOPVAAIDSN 600
Db 541 FSIYCGISIAHSLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDCIOPVAAIDSN 600
QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVYHNM 660
Db 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKKGYRDPVYHNM 660
QY 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
Db 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLHRTGNTNNSFOVASKSVLAALY 720
QY 721 SSEGSMERHHPAQAIATILNTHGNCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD 780
Db 721 SSEGSMERHHPAQAIATILNTHGNCNIFDHFSSKDYQRMMLDMRDIIILATDLAHLRIFKD 780
QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLK 840

Db 781 LQKMAEVDYRTNKHSHLLCLLMTSCDLSQYKWKTKTKIAELIYKEFFSQGLDLEKA 840
Qy 841 MGNRPMMMDREKAYIPBLQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 841 MGNRPMMMDREKAYIPBLQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900
Qy 901 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 942

RESULT 4

US-08-479-532-43
; Sequence 43, Application US/08479532
; Patent No. 576752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 576752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-532-43

Query Match 100.0%; Score 4911; DB 1; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGQACGHILCRSQYPAARPAERPGQVFLKPDEPPPPPPPCADSLQDALLSLGSLVDV 60
Db 1 MGQACGHILCRSQYPAARPAERPGQVFLKPDEPPPPPPPCADSLQDALLSLGSLVDV 60
Qy 61 AGLQQAKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOEGKVRVAVISRKRLGCN 120

Db 61 AGLQQAKEALSAVLPKVTYTYLLDGSRLVCEPPHELPOEGKVRVAVISRKRLGCN 120
Qy 121 GLGSPDLPGKPLARLVAFLAPDQTQVILPLVDKEAGAAVAVILVHCQOLSNEWSLQAV 180
Db 121 GLGSPDLPGKPLARLVAFLAPDQTQVILPLVDKEAGAAVAVILVHCQOLSNEWSLQAV 180
Qy 181 EKHTLVALKRVQALQOQRESSVAPETQNPPEAAGDQGGVAYTDQDKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPETQNPPEAAGDQGGVAYTDQDKILQLCGELYDL 240
Qy 241 DASSLQQLKVLQYLQOQETQASRCCLLLVSDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV 300
Db 241 DASSLQQLKVLQYLQOQETQASRCCLLLVSDNLQLSCKVIGDKVLEEEISFPLTTGRLQGV 300
Qy 301 VEDKKSITQLKDLTSEDNQOLQSMGLGCEVQAMLCPVVISRATDQVVALACAFNKLGDDLFT 360
Db 301 VEDKKSITQLKDLTSEDNQOLQSMGLGCEVQAMLCPVVISRATDQVVALACAFNKLGDDLFT 360
Qy 361 DQDEHVIQHCPTHYSTVLTTSTLAFQKQKQKCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQDEHVIQHCPTHYSTVLTTSTLAFQKQKQKCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
Qy 481 DAYAHLPLFYRGVDDSTGFRTRNILCFPIKQENQVIGVAELVNKINGPWFPSKFDDELATA 540
Db 481 DAYAHLPLFYRGVDDSTGFRTRNILCFPIKQENQVIGVAELVNKINGPWFPSKFDDELATA 540
Qy 541 PSYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
Db 541 PSYCGISIAHSLLYKKVNEAQYRSHLANEMMMTHMKVSDDEYTKLLHDGQIPVAAIDSN 600
Qy 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTTLARFCLMVKKGYRDPYHNWM 660
Db 601 FASFTYTPRSIPEDDTSMAILSMLQDMNFNNYKIDCPTTLARFCLMVKKGYRDPYHNWM 660
Qy 661 HAFSVSHFCYLLYKNLEITNYLEDMEIFALPISCMCHDLHRGTNNSPQVASKSVLAALY 720
Db 661 HAFSVSHFCYLLYKNLEITNYLEDMEIFALPISCMCHDLHRGTNNSPQVASKSVLAALY 720
Qy 721 SSEGSMVRRHFAQAIAILNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRIKPD 780
Db 721 SSEGSMVRRHFAQAIAILNTHGNCIFDHFGRKDYQRMLDLMDRIILATDLAHLRIKPD 780
Qy 781 LQKMAEVDYRTNKHSHLLCLLMTSCDLSQYKWKTKTKIAELIYKEFFSQGLDLEKA 840
Db 781 LQKMAEVDYRTNKHSHLLCLLMTSCDLSQYKWKTKTKIAELIYKEFFSQGLDLEKA 840
Qy 841 MGNRPMMMDREKAYIPBLQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 841 MGNRPMMMDREKAYIPBLQISFMEHIAMPYIKLLQDLFPKAAELYERVASNRHWTKVS 900
Qy 901 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDLDEEYVDPDLCARAPINGCCSLDAE 942

RESULT 5

US-08-455-526-43
; Sequence 43, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

```
/
/ ADDRESS: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 31-MAY-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/297,494
/ FILING DATE: 29-AUG-1994
/ APPLICATION NUMBER: US 07/688,356
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5789553and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30822
/ TELEPHONE: (312) 346-5750
/ TELEFAX: (312) 984-9740
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 43:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 942 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
/ US-08-455-526-43
/
/ Query Match 100.0%; Score 4911; DB 1; Length 942;
/ Best Local Similarity 100.0%; Pred. No. 0;
/ Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
/
/ QY 1 MQQACGHSILCSQQYPAARPAEPGRQQVFLKPDPPPPPPPCADSLQDALLSLGSDIV 60
/ DB 1 MQQACGHSILCSQQYPAARPAEPGRQQVFLKPDPPPPPPPCADSLQDALLSLGSDIV 60
/
/ QY 61 AGLOQAVKEALSAPVKVETVYLLDGSRLVCEPPEHLPQEGKVRKRLG 120
/ DB 61 AGLOQAVKEALSAPVKVETVYLLDGSRLVCEPPEHLPQEGKVRKRLG 120
/
/ QY 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVLVHCGQLSDNEEWSLQAV 180
/ DB 121 GLGPSDLPGKPLARLVAPLAPDTQVLVPLVDKEAGAAVAVLVHCGQLSDNEEWSLQAV 180
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/ QY 181 EKHTLVAKRVQALQOQRESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQCGELYDL 240
/ DB 181 EKHTLVAKRVQALQOQRESSVAPEATQNPPEAAGDQKGVAYTDQDRKILQCGELYDL 240
/
/ QY 241 DASSILQKVLQLOQEQASRCCLLVSDNLQSKVIGDKVBEETSPFLTTRGLGV 300
/ DB 241 DASSILQKVLQLOQEQASRCCLLVSDNLQSKVIGDKVBEETSPFLTTRGLGV 300
/
/ QY 301 VEDKKSIOQLKDTSEDQMLGCEVQAMLCVPIVRATDQVVALACAFNKLGGDLFT 360
/ DB 301 VEDKKSIOQLKDTSEDQMLGCEVQAMLCVPIVRATDQVVALACAFNKLGGDLFT 360
/
/ QY 361 DQDEHVIQCHFTYSTVLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420
/ DB 361 DQDEHVIQCHFTYSTVLSTLAFQKEQKLCCEQALLQVAKNLFTHLDDVSVLQEIIT 420
/
/ QY 421 EARNLSNABICSVFLDDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
/ DB 421 EARNLSNABICSVFLDDQNELVAKVFDGGVVEDESYEIRIPADQGIAGHVATTGQILNIP 480
/
/ QY 481 DAYAHLFYRGVDDSTGTRTRNLCFPKINENQEVIGVAELVKNKINGPWFSPKDEDLATA 540
/ DB 481 DAYAHLFYRGVDDSTGTRTRNLCFPKINENQEVIGVAELVKNKINGPWFSPKDEDLATA 540
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/ QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDDYTKLLHDGIGOPVAAIDSN 600
/ DB 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDDYTKLLHDGIGOPVAAIDSN 600
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/ QY 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNM 660
/ DB 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFNNYKIDCPTLARFCLMVKGYRDPYPYHNM 660
/
/ QY 661 HAFVSHEFCYLLYKNLELTNYLEDMEIFALFISCHDLDRGTNNSPQVASKSVLAALY 720
/ DB 661 HAFVSHEFCYLLYKNLELTNYLEDMEIFALFISCHDLDRGTNNSPQVASKSVLAALY 720
/
/ QY 721 SSEGSVMERHHPAQAIALNTHGNCNIPDFHSRKYQRMFLMRDILLATDLAHLRIFKD 780
/ DB 721 SSEGSVMERHHPAQAIALNTHGNCNIPDFHSRKYQRMFLMRDILLATDLAHLRIFKD 780
/
/ QY 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840
/ DB 781 LQKMAEVGYDRTNKQHSLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840
/
/ QY 841 MGNRPMENMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900
/ DB 841 MGNRPMENMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900
/
/ QY 901 HKFTIRGLPSNNSLDPLDEEYEVDPDLCGARAPINGCCSLDAE 942
/ DB 901 HKFTIRGLPSNNSLDPLDEEYEVDPDLCGARAPINGCCSLDAE 942
/
/ RESULT 6
/ US-08-455-525-43
/ Sequence 43, Application US/08455525
/ Patent No. 5800987
/ GENERAL INFORMATION:
/ APPLICANT: Beavo, Joseph A.
/ APPLICANT: Bentley, Kelley
/ APPLICANT: Charbonneau, Harry
/ APPLICANT: Sonnenburg, William K.
/ TITLE OF INVENTION: DNA Encoding Mammalian
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ ADDRESSEE: Bicknell
/ STREET: Two First National Plaza, 20 South Clark
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ FILING DATE: 31-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/297,494
/ FILING DATE:
/ APPLICATION NUMBER: US 07/688,356
/ FILING DATE: 04-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 5800987and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 27866/30822
/ TELECOMMUNICATION INFORMATION:
```


Db 121 GIGPSDLPKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQSDNEWSLQAV 180
Qy 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDGQKGVAYTTQDQKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDGQKGVAYTTQDQKILQLCGELYDL 240
Qy 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLGV 300
Db 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLGV 300
Qy 301 VEDKKSIOQLKDLTSEDQMLQSGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSIOQLKDLTSEDQMLQSGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Qy 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
Db 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
Qy 421 EARNLSNABEICSVFLLDQNELVAKVDPGGVDESYEIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABEICSVFLLDQNELVAKVDPGGVDESYEIRIPADQGIAGHVATTGQILNIP 480
Qy 481 DAYAHLPLFRGVDDSTGFRTRNLCPPIKVENQOEIVGVAELVKNKINGPWFSEFDEDLATA 540
Db 481 DAYAHLPLFRGVDDSTGFRTRNLCPPIKVENQOEIVGVAELVKNKINGPWFSEFDEDLATA 540
Qy 541 PSYICGISTAHSLLYKKNVACVRSHLANEMMMYHMKVSDDEYTKLLHDGIDPVAADISN 600
Db 541 PSYICGISTAHSLLYKKNVACVRSHLANEMMMYHMKVSDDEYTKLLHDGIDPVAADISN 600
Qy 601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPHNM 660
Db 601 PASFTYTPRSLPDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPHNM 660
Qy 661 HAFSVSHFCYLYKNLENTYLEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
Db 661 HAFSVSHFCYLYKNLENTYLEMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
Qy 721 SSEGSMERHHPAQAIILNTHGNCIFDHSRKYORMLDMLDRDILATDLAHLRIPKD 780
Db 721 SSEGSMERHHPAQAIILNTHGNCIFDHSRKYORMLDMLDRDILATDLAHLRIPKD 780
Qy 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840
Db 781 LQKMAEVGYDRNKHSHLLCLLMTSCDLSQTKGWKTRKIAELIYKEFFSQGDLEKA 840
Qy 841 MGNRRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900
Db 841 MGNRRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLPPKAAELYERVASNREHWTKVS 900
Qy 901 HKFTIRGLPSNNSLDFLDEYEVDPDLGARABINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDFLDEYEVDPDLGARABINGCCSLDAE 942

RESULT 8

US-09-883-825-43
; Sequence 43, Application US/09883825
; Patent No. 6642040
; GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark
Street

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6642040and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-883-825-43

Query Match 100.0%; Score 4911; DB 4; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQAGCHSILCRSQYPAARPAEPGRQGVFLKDPDEPPPPQPCADSLQDALLSLGSVIDV 60
Db 1 MQAGCHSILCRSQYPAARPAEPGRQGVFLKDPDEPPPPQPCADSLQDALLSLGSVIDV 60
Qy 61 AGLOQAVKEALSAPLVKPVETVYLLDGESRLVCEEPHELPQEGKVRNAVSRKRLGCN 120
Db 61 AGLOQAVKEALSAPLVKPVETVYLLDGESRLVCEEPHELPQEGKVRNAVSRKRLGCN 120
Qy 121 GLGPSDLPGKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQSDNEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAPLADPTQVLVPLVDKEGAVAAVILVHCGQSDNEWSLQAV 180
Qy 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDGQKGVAYTTQDQKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPEATQNPPEEAGDGQKGVAYTTQDQKILQLCGELYDL 240
Qy 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLGV 300
Db 241 DASSLQKLVQYLOQETOASRCCLLVSDNQLQSKVIGDKVLEBEEISFPITTRGLGV 300
Qy 301 VEDKKSIOQLKDLTSEDQMLQSGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 301 VEDKKSIOQLKDLTSEDQMLQSGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Qy 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
Db 361 DQDEHVIQHCFTYTSVLTLSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
Qy 421 EARNLSNABEICSVFLLDQNELVAKVDPGGVDESYEIRIPADQGIAGHVATTGQILNIP 480
Db 421 EARNLSNABEICSVFLLDQNELVAKVDPGGVDESYEIRIPADQGIAGHVATTGQILNIP 480

QY 481 DAYAHPLFYRGVDDSTGFRTRNLCFPKIQNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540
DB |||||
QY 481 DAYAHPLFYRGVDDSTGFRTRNLCFPKIQNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540
DB |||||
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIGPVAADSN 600
DB |||||
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIGPVAADSN 600
DB |||||
QY 601 FASFTYTPRSLPEDDTSMAILSMQDMNF INNYKIDCPTLARFCLMWKKGVRDPPYHNM 660
DB |||||
QY 601 FASFTYTPRSLPEDDTSMAILSMQDMNF INNYKIDCPTLARFCLMWKKGVRDPPYHNM 660
DB |||||
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720
DB |||||
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720
DB |||||
QY 721 SSEGSVMERHHPAQAIALNTHGNCIFDHFGRKDYQRMOLDLMDRIILATDLAHLRI PKD 780
DB |||||
QY 721 SSEGSVMERHHPAQAIALNTHGNCIFDHFGRKDYQRMOLDLMDRIILATDLAHLRI PKD 780
DB |||||
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
DB |||||
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
DB |||||
QY 841 MGNRPMMMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
DB |||||
QY 841 MGNRPMMMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
DB |||||
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDGGARAPINGCCSLDAE 942
DB |||||
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDGGARAPINGCCSLDAE 942
DB |||||

RESULT 9

PCT-US92-03222-43
; Sequence 43, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03222
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-03222-43

Query Match 100.0%; Score 4911; DB 5; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGQACGSHILCRSQYPAARPAEPGRQOVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
DB |||||
QY 1 MGQACGSHILCRSQYPAARPAEPGRQOVFLKPDPEPPPPQPCADSLQDALLSLGSDIV 60
DB |||||
QY 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEPPHPELPQEGKVREAVISRKLGCN 120
DB |||||
QY 61 AGLOQAVKEALSAVLPKVTETVYLLDGESRLVCEPPHPELPQEGKVREAVISRKLGCN 120
DB |||||
QY 121 GLGPSDLPGKELARLAPADPTQVLYPLVDKAGAAVAVILVHCGQLSNEEWSLOAV 180
DB |||||
QY 121 GLGPSDLPGKELARLAPADPTQVLYPLVDKAGAAVAVILVHCGQLSNEEWSLOAV 180
DB |||||
QY 181 EKHTLVALKRQALQORESSVAPEATQNPPEAAAGDQKGVAYTDQDRKILQLCGELYDL 240
DB |||||
QY 181 EKHTLVALKRQALQORESSVAPEATQNPPEAAAGDQKGVAYTDQDRKILQLCGELYDL 240
DB |||||
QY 241 DASSLQLKVLQYLOOETOASRCCLLLVSEDNLQLSCKVIGDKVLEETISFPLTTGRLQGV 300
DB |||||
QY 241 DASSLQLKVLQYLOOETOASRCCLLLVSEDNLQLSCKVIGDKVLEETISFPLTTGRLQGV 300
DB |||||
QY 301 VEDKKSQQLKDLTSEDMOQLQSMGCEVQAMLCVPVTSRATDQVVALACAFNKGGLDFT 360
DB |||||
QY 301 VEDKKSQQLKDLTSEDMOQLQSMGCEVQAMLCVPVTSRATDQVVALACAFNKGGLDFT 360
DB |||||
QY 361 DQDEHVIQCHPHYTSTVLTSFLAFQKQKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
DB |||||
QY 361 DQDEHVIQCHPHYTSTVLTSFLAFQKQKCEQALLQVAKNLFTHLDDVSVLQEIIT 420
DB |||||
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGCVVDESEYIRIPADQGIAGHVATTGQILNIP 480
DB |||||
QY 421 EARNLSNAEICSVFLLDQNELVAKVFDGCVVDESEYIRIPADQGIAGHVATTGQILNIP 480
DB |||||
QY 481 DAYAHPLFYRGVDDSTGFRTRNLCFPKIQNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540
DB |||||
QY 481 DAYAHPLFYRGVDDSTGFRTRNLCFPKIQNEQEVIGVAELVKNKINGPWFSKFDEDLATA 540
DB |||||
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIGPVAADSN 600
DB |||||
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMMYHKVSDDEYTKLLHDGIGPVAADSN 600
DB |||||
QY 601 FASFTYTPRSLPEDDTSMAILSMQDMNF INNYKIDCPTLARFCLMWKKGVRDPPYHNM 660
DB |||||
QY 601 FASFTYTPRSLPEDDTSMAILSMQDMNF INNYKIDCPTLARFCLMWKKGVRDPPYHNM 660
DB |||||
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720
DB |||||
QY 661 HAFSVSHFCYLLYKNLELTNYLEDMEIPALFISCMCHDLHRGTNNSQVASKSVLAALY 720
DB |||||
QY 721 SSEGSVMERHHPAQAIALNTHGNCIFDHFGRKDYQRMOLDLMDRIILATDLAHLRI PKD 780
DB |||||
QY 721 SSEGSVMERHHPAQAIALNTHGNCIFDHFGRKDYQRMOLDLMDRIILATDLAHLRI PKD 780
DB |||||
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
DB |||||
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWTKTKIAELIYKEFFSQGDLEKA 840
DB |||||
QY 841 MGNRPMMMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
DB |||||
QY 841 MGNRPMMMDREKAYIPELOISFMEHIAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
DB |||||
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDGGARAPINGCCSLDAE 942
DB |||||

Db 901 HKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPINGCCSLDAE 942

RESULT 10
US-07-872-644-45
; Sequence 45, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,644
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
Qy 1 MQACGHSILCRSQYPAARPAERGGQVFLKPDPPPPPPQPCADSLDALLSLGSDIV 60
Db 1 MQACGHSILCRSQYPAARPAERGGQVFLKPDPPPPPPQPCADSLDALLSLGSDIV 60
Qy 61 AGLOQAVKEALSAPLVKVTYVTVYLLDGESESLVCEPPHPELQEGKREAVISRKLGCN 120
Db 61 SGLQRAVKEALSAPLVKVTYVTVYLLDGESESLVCEPPHPELQEGKREAVISRKLGCN 120
Qy 121 GLGPSDLPGKPLARLVAIPADTVLPLVDKAGAAVAVLHVCGQLSNEEWSLOAV 180
Db 121 GLGPSDLPGKPLARLVAIPADTVLPLVDKAGAAVAVLHVCGQLSNEEWSLOAV 180
Qy 181 EKHTLVALKRVQALQORESSVAPEATONPPPEAAGQKGVAYTDDDRKILQLCGELYDL 240
Db 181 EKHTLVALLRRVQLOQRGAPRAVONPPPEGTAEDQKGAAYTDDDRKILQLCGELYDL 240

Qy 241 DASSLQLKVLQYLOQETOASRCCLLLVSDNLIQLSCKVIGDKVLEETISFPLTTGRLGV 300
Db 241 DASSLQLKVLQYLOQETOASRCCLLLVSDNLIQLSCKVIGDKVLEETISFPLTTGRLGV 299
Qy 301 VEDKKSIOQLKDLTSDMOQLOSLMGLCEVOAMLCVPIVIRATDQVVALACAFNKLGGDLFT 360
Db 300 VEDKKSIOQLKDLTSDMOQLOSLMGLCEVOAMLCVPIVIRATDQVVALACAFNKLGGDLFT 359
Qy 361 DODEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 420
Db 360 DODEHVIQHCFTYTSVLTSTLAFQKEQKLKCECQALLQVAKNLFTHLDDVSVLQEIIT 419
Qy 421 EARNLSNAEICSVFLDDQNELVAKVFDGCVVEDESEYIRIPADQIAGHAVTGGIINLP 480
Db 420 EARNLSNAEICSVFLDDQNELVAKVFDGCVVEDESEYIRIPADQIAGHAVTGGIINLP 479
Qy 481 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQNEVIGVAELVKNKINGPMFSGFDEDLATA 540
Db 480 DAYAHPFLYRGVDDSTGFRTRNLCFPIKNEQNEVIGVAELVKNKINGPMFSGFDEDLATA 539
Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIIQPVAAIDSN 600
Db 540 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIIQPVAAIDSN 599
Qy 601 PASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMM 660
Db 600 PASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKIDCPTLARFCLMVKKGYRDPYHNMM 659
Qy 661 HAFVSVSHFCYLLYKNLELTNYLDEMEIFALFTSCMCHDLDRGTNNNSFOVASKSLAALY 720
Db 660 HAFVSVSHFCYLLYKNLELTNYLDEMEIFALFTSCMCHDLDRGTNNNSFOVASKSLAALY 719
Qy 721 SSEGSMERHFAQAIAILNTHGNCIFDHSRKOYQRMLDLMDRIILATDLAHLRIKFD 780
Db 720 SSEGSMERHFAQAIAILNTHGNCIFDHSRKOYQRMLDLMDRIILATDLAHLRIKFD 779
Qy 781 LQKMAEVGYDRNKKOHHLLCLLMTSCDLSQDTQGWTKTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKKOHHLLCLLMTSCDLSQDTQGWTKTRKIAELIYKEFFSQGDLEKA 839
Qy 841 MGNRPMENMDREKAYIPELOISFMHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
Db 840 MGNRPMENMDREKAYIPELOISFMHIAPIYKLLQDLFPKAAELYERVASNREHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYEVDPDLDGARAPINGCCSLDAE 941

RESULT 11
US-08-297-494-45
; Sequence 45, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/297,494
FILING DATE: 04-APR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 558077land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-494-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQACGSHILCSQQYPAARPAERGGQVFLKPEPPPPPPPCADSLQDALLSLGSLVIDV 60
Db 1 MQACGSHILCSQQYPAARPAERGGQVFLKPEPPPPPPPCADSLQDALLSLGSLVIDI 60

Qy 61 AGLOAVKEALSAPLKVETVYVYLLDGEESRLVCEPPHLPQEGKREAVISRKLGCN 120
Db 61 SGLQRAVKEALSAPLKVETVYVYLLDGEESRLVCEPPHLPQEGKREAVISRKLGCN 120

Qy 121 GLGSDLPKGLARLVAFLADPTQVLPVVDKEAGAAVAVILVHCGQLSNEWSLQAV 180
Db 121 GLGSDLPKGLARLVAFLADPTQVLPVVDKEAGAAVAVILVHCGQLSNEWSLQAV 180

Qy 181 EKHTLVALKRVQALQORESSVAPATONPPPEAGDQKGVAYTDDQRKILQLCGELYDL 240
Db 181 EKHTLVALKRVQALQORESSVAPATONPPPEAGDQKGVAYTDDQRKILQLCGELYDL 240

Qy 241 DASSLQLKVLQYLOQETQASRCLLLVSEDLNLQLSCKVIGDKVLEELISFPLTTGRLGQV 300
Db 241 DASSLQLKVLQYLOQETQASRCLLLVSEDLNLQLSCKVIGDKVLEELISFPLTTGRLGQV 299

Qy 301 VEDKKSIOQLKDLTSEDVQOQSMGLGCEVOAMLCVPVISRATDQVVALACAFNKGGLFT 360
Db 300 VEDKKSIOQLKDLTSEDVQOQSMGLGCEVOAMLCVPVISRATDQVVALACAFNKGGLFT 359

Qy 361 DODEHVIQCHFYTSVLTSTLAFOKEQKLKCEQALLQVAKNLFTHLDDVSVLLQELIT 420
Db 360 DODEHVIQCHFYTSVLTSTLAFOKEQKLKCEQALLQVAKNLFTHLDDVSVLLQELIT 419

Qy 421 EARLNSNAEICSVFLDDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTQOILNIP 480
Db 420 EARLNSNAEICSVFLDDQNELVAKVFDGGVVEDESEYIRIPADQGIAGHVATTQOILNIP 479

Qy 481 DAYAHLPIYRGVDDSTGFRTRNLCFPPIKNEQVIGVAVELVNKINGPWFSKFDEDLATA 540
Db 480 DAYAHLPIYRGVDDSTGFRTRNLCFPPIKNEQVIGVAVELVNKINGPWFSKFDEDLATA 539

Qy 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMWYHMKVSDDEYTKLLHDGQIPVAADSN 600
Db 540 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMWYHMKVSDDEYTKLLHDGQIPVAADSN 599

Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCMLVKKGYRDPYPYHNM 660
Db 600 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCMLVKKGYRDPYPYHNM 659

661 HAPSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 720
Db 660 HAPSVSHFCYLLYKNLELTNYLEDIEIFALFISCMCHDLDRGTNNNSFOVASKSVLAALY 719

Qy 721 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSSKDYQRMQLDMRDIIILATDLAHLRIFKD 780
Db 720 SSEGSMERHHFAQAIAILNTHGNCNIFDHFSSKDYQRMQLDMRDIIILATDLAHLRIFKD 779

Qy 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEYGYDRNNKQHRLLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLEKA 839

Qy 841 MGNRPMBMDREKAYIPELQISFMEHIAMPTIKLQDLFPKAAELYERVASNRHHTWKVS 900
Db 840 MGNRPMBMDREKAYIPELQISFMEHIAMPTIKLQDLFPKAAELYERVASNRHHTWKVS 899

Qy 901 HKFTIRGLPSNNSLDLDEEYVDPDLGAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDLDEEYVDPDLGAPINGCCSLDAE 941

RESULT 12
US-08-297-510-45
Sequence 45, Application US/08297510
Patent No. 5602019
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-510-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGHSILCRSQYPAARPAARPGQVFLKPDDEPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MGQACGHSILCRSQYPAARPAARPGQVFLKPDDEPPPPPPQCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVSRKELG 120
Db 61 SGLQRAVKALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVSRKELG 120
QY 121 GLGPSDLPGKPLARLVAFLAPDTQVLPVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDTQVLPVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVAQLQORESSVAPEATONPPPEAAGQKGVAVYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVAQLQORESSVAPEATONPPPEAAGQKGVAVYTDQDRKILQCGELYDL 240
QY 241 DASSLQKLVQLQOETASRCCLLVSDNLQSLCKVIGDKVLEESIFPLTTGRLGV 300
Db 241 DASSLQKLVQLQOETASRCCLLVSDNLQSLCKVIGDKVLEESIFPLTTGRLGV 300
QY 301 VEDKKSILQKDLTSEDVQQLQSMGLCELQAMLCVPVISRATQOVVALACAFNKLGGDLFT 360
Db 301 VEDKKSILQKDLTSEDVQQLQSMGLCELQAMLCVPVISRATQOVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIIT 420
QY 421 EARNLSNABICSVFLDQNELVAKVDPGGVDESEYIRIPADQIAGHVAATGQILNP 480
Db 421 EARNLSNABICSVFLDQNELVAKVDPGGVDESEYIRIPADQIAGHVAATGQILNP 480
QY 481 DAYAHPFLYRGVDDSTGFRNLCPPIKNEQVIGVAVELVKNKINGPWFSDDEDLATA 540
Db 481 DAYAHPFLYRGVDDSTGFRNLCPPIKNEQVIGVAVELVKNKINGPWFSDDEDLATA 540
QY 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQFVAIDSN 600
Db 541 FSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQFVAIDSN 600
QY 601 FASFTYTPRSLPDDTSMALSMQDMFNINNYKIDCPTLAFCLMVKKGYRDPYHNM 660
Db 601 FASFTYTPRSLPDDTSMALSMQDMFNINNYKIDCPTLAFCLMVKKGYRDPYHNM 660
QY 661 HAFVSHPFCVLYKNELENYLEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALY 720
Db 661 HAFVSHPFCVLYKNELENYLEDMEIFALFISCMCHDLDRGTNNSFOVASKSVLAALY 720
QY 721 SSEGSMERHHPFAQAIATLNTGNCNIFDHSRKYQRMDLMDRIILATDLAHLRIK 780
Db 721 SSEGSMERHHPFAQAIATLNTGNCNIFDHSRKYQRMDLMDRIILATDLAHLRIK 780
QY 781 LQMAEVGVDRNKHSHLLCLLMTSCDLSDQTKGWKTRKIAELIYKEFFSQGDLEKA 840
Db 781 LQMAEVGVDRNKHSHLLCLLMTSCDLSDQTKGWKTRKIAELIYKEFFSQGDLEKA 840
QY 841 MGNRPWEMMDREKAVIPELQISFMEHIAPIYKLDLPKPAELYERVASRHHWTKVS 900
Db 841 MGNRPWEMMDREKAVIPELQISFMEHIAPIYKLDLPKPAELYERVASRHHWTKVS 900
QY 901 HKFTIRGLPSNNSLDPLDEYEVDPDLGAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDPLDEYEVDPDLGAPINGCCSLDAE 942

RESULT 13

US-08-479-532-45
; Sequence 45, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley

APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSES: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,532
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5776752and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLESCULE TYPE: protein
US-08-479-532-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;

Best Local Similarity 96.0%; Pred. No. 0;

Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

QY 1 MGQACGHSILCRSQYPAARPAARPGQVFLKPDDEPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MGQACGHSILCRSQYPAARPAARPGQVFLKPDDEPPPPPPQCADSLQDALLSLGSDIV 60
QY 61 AGLOQAVKEALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVSRKELG 120
Db 61 SGLQRAVKALSAVLPKVTYVTVLLDGSRLVCEPPELPOEGKVRVAVSRKELG 120
QY 121 GLGPSDLPGKPLARLVAFLAPDTQVLPVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAFLAPDTQVLPVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVAQLQORESSVAPEATONPPPEAAGQKGVAVYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVAQLQORESSVAPEATONPPPEAAGQKGVAVYTDQDRKILQCGELYDL 240
QY 241 DASSLQKLVQLQOETASRCCLLVSDNLQSLCKVIGDKVLEESIFPLTTGRLGV 300
Db 241 DASSLQKLVQLQOETASRCCLLVSDNLQSLCKVIGDKVLEESIFPLTTGRLGV 300
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Db 301 VEDKKSILQKDLTSEDVQQLQSMGLCELQAMLCVPVISRATQOVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQCHFYHTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQEIIT 420

[illegible]

QY 781 LQMAEVGYDRTNKHQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLXA 840
DB 780 LQMAEVGYDRTNKHQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLXA 839
QY 841 MGNRPMEWMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
DB 840 MGNRPMEWMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 899
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942
DB 900 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 941

RESULT 15

US-08-455-525-45
; Sequence 45, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,525
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5800987and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCES/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 941 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-525-45

Query Match 96.3%; Score 4728.5; DB 1; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;
QY 1 MQGACGHSILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60
DB 1 MQGACGHSILCSQQYPAARPAEPGRGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60

QY 61 AGLOQAVKEALSNAVLPKVETVYTYLLDGSRLVCEBPPHELPOEGKGVREAVISRKELGNC 120
DB 61 SGLQRAVKEALSNAVLPRVETVYTYLLDGSRLVCEBPPHELPOEGKGVREAVISRKELGNC 120
QY 121 GLGPSDLPGKPLARLAVAPLAPDTQVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
DB 121 GLGPSDLPGKPLARLAVAPLAPDTQVLVIPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
QY 181 EKHTLVALKRVQALQOORESSVAPEATQNPPEBAAGQKGGVAYTDDRKILQJCGELYDL 240
DB 181 EKHTLVALKRVQALQOORESSVAPEATQNPPEBAAGQKGGVAYTDDRKILQJCGELYDL 240
QY 241 DASSLQLKVLQYLQOETQASRCCLLVSEDNLQJCKVIGDKVLEBIEISFPLTTGRLGQV 300
DB 241 DASSLQLKVLQYLQOETQASRCCLLVSEDNLQJCKVIGDKVLEBIEISFPLTTGRLGQV 299
QY 301 VEDKKSIOQLKLTSDMOQLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 360
DB 300 VEDKKSIOQLKLTSDMOQLQSMGCEVQAMLCVPIVSRATQVVALACAFNKLGGDLFT 359
QY 361 DQDEHVIQHCPTHYSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIT 420
DB 360 DQDEHVIQHCPTHYSTVLTSTLAFQKEQKLKCEQALLQVAKNLFTHLDDVSVLLQEIT 419
QY 421 EARNLSNABEICSVFLLDQNELVAKVFDGCVVDESEYRIPADQGIAGHVATTGQILNIP 480
DB 420 EARNLSNABEICSVFLLDQNELVAKVFDGCVVDESEYRIPADQGIAGHVATTGQILNIP 479
QY 481 DAYAHPLFYRGVDDSTGFRTRNLCFPIKVENQEVIGVAELVNKINGPWFSPDEDLATA 540
DB 480 DAYAHPLFYRGVDDSTGFRTRNLCFPIKVENQEVIGVAELVNKINGPWFSPDEDLATA 539
QY 541 FSIYCGISIAHSLLYKKNYKNEAQRSHLANEMMYHMKVSDDEYTKLLHDIQPVAAIDSN 600
DB 540 FSIYCGISIAHSLLYKKNYKNEAQRSHLANEMMYHMKVSDDEYTKLLHDIQPVAAIDSN 599
QY 601 PASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPVHNM 660
DB 600 PASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKGYRDPYPVHNM 659
QY 661 HAPSVSHFCYLLYKXLELTNYLEDMEIFALFISCHDLDRGTNNSFOVASKSVLAALY 720
DB 660 HAPSVSHFCYLLYKXLELTNYLEDMEIFALFISCHDLDRGTNNSFOVASKSVLAALY 719
QY 721 SSEGSVMERHHPAQAIAILNTHGNCNIFDHFSSKDYQRMLDLMDIILATDLAHLRIFKD 780
DB 720 SSEGSVMERHHPAQAIAILNTHGNCNIFDHFSSKDYQRMLDLMDIILATDLAHLRIFKD 779
QY 781 LQMAEVGYDRTNKHQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLXA 840
DB 780 LQMAEVGYDRTNKHQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFFSQGDLXA 839
QY 841 MGNRPMEWMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 900
DB 840 MGNRPMEWMDREKAYIPELQISFMEHIAMPIYKLLQDLFPKAAELYERVASNREHWTKVS 899
QY 901 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 942
DB 900 HKFTIRGLPSNNSLDFLDEEYVDPDLGAPINGCCSLDAE 941

Search completed: June 26, 2005, 12:24:06
Job time : 34.8438 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	4911	100.0	942	9	US-09-883-825-43		Sequence 43, Appl
2	4911	100.0	942	16	US-10-697-894-43		Sequence 43, Appl
3	4728.5	96.3	941	9	US-09-883-825-45		Sequence 45, Appl
4	4728.5	95.3	941	16	US-10-697-894-45		Sequence 45, Appl
5	4728.5	96.3	941	16	US-10-686-390-5		Sequence 5, Appl
6	4728.5	96.3	941	17	US-10-686-282-5		Sequence 5, Appl
7	4728.5	96.3	941	17	US-10-686-349-5		Sequence 5, Appl
8	4657	94.8	921	9	US-09-883-825-39		Sequence 39, Appl
9	4657	94.8	921	13	US-10-094-889-5		Sequence 5, Appl
10	4657	94.8	921	16	US-10-697-894-39		Sequence 39, Appl
11	4530.5	92.3	905	13	US-10-094-989-4		Sequence 4, Appl

Sequence 78, Appl
Sequence 2, Appl
Sequence 2928, Ap
Sequence 2944, Ap
Sequence 30, Appl
Sequence 30, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 39, Appl
Sequence 14, Appl
Sequence 4, Appl
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Sequence 3, Appl
Sequence 23, Appl
Sequence 5, Appl
Sequence 1, Appl

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;
;
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27666/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-883-825-43

Query Match 100.0%; Score 4911; DB 9; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPOPCADSLQDALLSLGSDIV 60
DB 1 MGQACGHSILCRSQYPAARPAERGGQVFLKPDPEPPPOPCADSLQDALLSLGSDIV 60
QY 61 AGLQAAVKEALSAVLPKVETVYTYLLDGSRLVCEEPHPELPQBGKRVREAVISRKLGCN 120
DB 61 AGLQAAVKEALSAVLPKVETVYTYLLDGSRLVCEEPHPELPQBGKRVREAVISRKLGCN 120
QY 121 GLGSPDLPKPLARLAPLAPDTQVLPVLDKAGAAVAVILVHCGQLSNEBWSLQAV 180
DB 121 GLGSPDLPKPLARLAPLAPDTQVLPVLDKAGAAVAVILVHCGQLSNEBWSLQAV 180
QY 181 EKHTLVALKRVOALQORESSVAPATONPPPEAAGDQGGVAYTDQDKILQLCGELYDL 240
DB 181 EKHTLVALKRVOALQORESSVAPATONPPPEAAGDQGGVAYTDQDKILQLCGELYDL 240
QY 241 DASSILQLKVLQYLOQETOASRCCLLVSEDLNLQLSCKVIGKVLBEERISFPLTTGRLGQV 300
DB 241 DASSILQLKVLQYLOQETOASRCCLLVSEDLNLQLSCKVIGKVLBEERISFPLTTGRLGQV 300
QY 301 VEDKKSILQDLTSEDMOQLSMLGCEVQAMLCVPVVISRATDQVVALACAFNKLGGDLFT 360
DB 301 VEDKKSILQDLTSEDMOQLSMLGCEVQAMLCVPVVISRATDQVVALACAFNKLGGDLFT 360
QY 361 DQDEHVIQCHPHYTSTVLSTLAFQKEOKLCECOALLQVAKNLFTHLDDVSVLLQELIT 420
DB 361 DQDEHVIQCHPHYTSTVLSTLAFQKEOKLCECOALLQVAKNLFTHLDDVSVLLQELIT 420
QY 421 EARLNSNAEISCVFLLDQNELVAKVFDGCVVDESEYRIRPADQGIAGHVATTQGLNIP 480
DB 421 EARLNSNAEISCVFLLDQNELVAKVFDGCVVDESEYRIRPADQGIAGHVATTQGLNIP 480
QY 481 DAYAHLPIYRGVDDSTGPRTRNLCFPPIKNEQEVIGVAELVNKINGPWFSPKFDLATA 540
DB 481 DAYAHLPIYRGVDDSTGPRTRNLCFPPIKNEQEVIGVAELVNKINGPWFSPKFDLATA 540
QY 541 FSIYCGISIAHSLLYKKYNEAQYRSHLANEMWYHMKVSDDEYTKLHDGQPVAADSN 600
DB 541 FSIYCGISIAHSLLYKKYNEAQYRSHLANEMWYHMKVSDDEYTKLHDGQPVAADSN 600
QY 601 PASFTYTPRSLPEDDTSMAILSMQDMNFNNYKIDCPTLARFCIMVKKGYRDPYHNWM 660
DB 601 PASFTYTPRSLPEDDTSMAILSMQDMNFNNYKIDCPTLARFCIMVKKGYRDPYHNWM 660
QY 661 HAFVSHPCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSPQVASKSVLAALY 720
DB 661 HAFVSHPCYLLYKNLELTNYLEDMEIPALFISCMCHDLDRGTNNNSPQVASKSVLAALY 720
QY 721 SSEGSVMERHFAQAIALNTHGCVNIPDFHSRKYQRMQLDMLMRDILLATDLAHLRIFKD 780
;
;
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27666/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 942 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-697-894-43

Query Match 100.0%; Score 4911; DB 16; Length 942;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 942; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 721 SSEGSVMERHFAQAIALNTHGCVNIPDFHSRKYQRMQLDMLMRDILLATDLAHLRIFKD 780
QY 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFPFSGDLEKA 840
DB 781 LQKMAEYGYDRTNKQHSLLCLLMTSCDLSQDTKGWKTTRKIAELIYKEFPFSGDLEKA 840
QY 841 MGNRPMEHMDREKAYIPELQISFMEHIAPIYKLQDLFPKAAELYERVAENRHHWTQVS 900
DB 841 MGNRPMEHMDREKAYIPELQISFMEHIAPIYKLQDLFPKAAELYERVAENRHHWTQVS 900
QY 901 HKFTIRGLPSNNSLDFDEEYVDPDGDARAPINGCCSLDAE 942
DB 901 HKFTIRGLPSNNSLDFDEEYVDPDGDARAPINGCCSLDAE 942

RESULT 2
US-10-697-894-43
; Sequence 43, Application US/10697894
; Publication No. US20040126866A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; City: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/697,894
; FILING DATE: 30-Oct-2003
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,783
; FILING DATE: 28-July-1998
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27666/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-697-894-43
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Qy 1 MGACGHSILCRSQOYPAARPAEPRGOVFLKDPDEPPPPPCADSLQDALLSLGSDIVD 60
Db 1 MGACGHSILCRSQOYPAARPAEPRGOVFLKDPDEPPPPPCADSLQDALLSLGSDIVD 60
Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKRVAVISRRLGCGN 120
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKRVAVISRRLGCGN 120
Qy 121 GLGPSDLPGKPLARLVAPADPTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
Db 121 GLGPSDLPGKPLARLVAPADPTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180
Qy 181 EKHTLVALKRVQALQOQRESSVAPATONPPEEAGDQKGVAYTDQDRKILQCGELYDL 240
Db 181 EKHTLVALKRVQALQOQRESSVAPATONPPEEAGDQKGVAYTDQDRKILQCGELYDL 240
Qy 241 DASSLQKLVQYLQOQSTOASRCCLLVSDNLQSLCKVIGDKVLEBIEISFPLTTGRGQV 300
Db 241 DASSLQKLVQYLQOQSTOASRCCLLVSDNLQSLCKVIGDKVLEBIEISFPLTTGRGQV 300
Qy 301 VEDKXSIQKDLTSEDMDQOQSLGMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
Db 301 VEDKXSIQKDLTSEDMDQOQSLGMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
Qy 361 DQEHVIOHCFTYTTSTLTAFQKEQKLKCEQALQVAKNLFTHLDDVSVLLQEIIT 420
Db 361 DQEHVIOHCFTYTTSTLTAFQKEQKLKCEQALQVAKNLFTHLDDVSVLLQEIIT 420
Qy 421 EARNLSNABICSVFLDDQNELVAKVFDGGVGEDESVEIRIPADQGIAGHVATTGQLNIP 480
Db 421 EARNLSNABICSVFLDDQNELVAKVFDGGVGEDESVEIRIPADQGIAGHVATTGQLNIP 480
Qy 481 DAYAHLFVRGDDSTGFRNLCFPKINENQEVIGVAELVKNKINGWFSDLDLATA 540
Db 481 DAYAHLFVRGDDSTGFRNLCFPKINENQEVIGVAELVKNKINGWFSDLDLATA 540
Qy 541 PSYCGISIAHSLLYKKNVQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
Db 541 PSYCGISIAHSLLYKKNVQYRSHLANEMMYHMKVSDDEYTKLLHDGIQPVAAIDSN 600
Qy 601 FASFTYTPRSPLPDDTSMALLSMLQDMFINNYKIDCPTLARFCLMWKGYRDPYHNM 660
Db 601 FASFTYTPRSPLPDDTSMALLSMLQDMFINNYKIDCPTLARFCLMWKGYRDPYHNM 660
Qy 661 HAFSVSHFCYLLKXNLENTYLEDMEIFALFTSCMCHDLDRGTNNSTFOVASKSVLAALY 720
Db 661 HAFSVSHFCYLLKXNLENTYLEDMEIFALFTSCMCHDLDRGTNNSTFOVASKSVLAALY 720
Qy 721 SSEGSVMERHHPAQAIALNTHGNCNIFDHSRKYQRMLDLMDRDIILATDLAHLRIFKD 780
Db 721 SSEGSVMERHHPAQAIALNTHGNCNIFDHSRKYQRMLDLMDRDIILATDLAHLRIFKD 780
Qy 781 LQKMAEVDYRNTKQHSLLCLLMTSCDLSQDTGKWTTRKIALBIYKEFFSQGDLEKA 840
Db 781 LQKMAEVDYRNTKQHSLLCLLMTSCDLSQDTGKWTTRKIALBIYKEFFSQGDLEKA 840
Qy 841 MGNRMWEMMDREKAYIPELOISFMESHAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 841 MGNRMWEMMDREKAYIPELOISFMESHAMPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
Db 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
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RESULT 3

US-09-883-825-45
; Sequence 45, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley

```
Charbonneau, Harry  
Sonnenburg, William K.  
TITLE OF INVENTION: DNA Encoding Mammalian  
Phosphodiesterases  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
Bicknell  
Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/883,825  
FILING DATE: 18-Jun-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/123,783  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/297,494  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 07/688,356  
FILING DATE: 04-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: NO. US20020151024A1and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30822  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 941 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-09-883-825-45
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Query Match 96.3%; Score 4728.5; DB 9; Length 941;  
Best Local Similarity 96.0%; Pred. No. 0;  
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 MGACGHSILCRSQOYPAARPAEPRGOVFLKDPDEPPPPPCADSLQDALLSLGSDIVD 60  
Db 1 MGACGHSILCRSQOYPAARPAEPRGOVFLKDPDEPPPPPCADSLQDALLSLGSDIVD 60  
Qy 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKRVAVISRRLGCGN 120  
Db 61 AGLOQAVKEALSAVLPKVTETVYLLDGSRLVCEPPHPELQEGKRVAVISRRLGCGN 120  
Qy 121 GLGPSDLPGKPLARLVAPADPTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180  
Db 121 GLGPSDLPGKPLARLVAPADPTQVLVPLVDKEAGAAVAVILVHCGQLSDNEEWSLQAV 180  
Qy 181 EKHTLVALKRVQALQOQRESSVAPATONPPEEAGDQKGVAYTDQDRKILQCGELYDL 240  
Db 181 EKHTLVALKRVQALQOQRESSVAPATONPPEEAGDQKGVAYTDQDRKILQCGELYDL 240  
Qy 241 DASSLQKLVQYLQOQSTOASRCCLLVSDNLQSLCKVIGDKVLEBIEISFPLTTGRGQV 300  
Db 241 DASSLQKLVQYLQOQSTOASRCCLLVSDNLQSLCKVIGDKVLEBIEISFPLTTGRGQV 300  
Qy 301 VEDKXSIQKDLTSEDMDQOQSLGMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360  
Db 301 VEDKXSIQKDLTSEDMDQOQSLGMLGCEVQAMLCVPVISRATQVVALACAFNKLGGDLFT 360
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Db 660 HAFSVSHFCYLLYKNLENTYLEDIEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 719
Qy 721 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIFKD 780
Db 720 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIFKD 779
Qy 781 LQKMAEVGYDRNKKOHSILLCMLTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKKOHSILLCMLTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 839
Qy 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVPLDGDTRAPINGCCSLDAE 941

RESULT 5
US-10-686-390-5
; Sequence 5, Application US/10686390
; Publication No. US20040254153A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343B
; CURRENT APPLICATION NUMBER: US/10/686,390
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-390-5

Query Match 96.3%; Score 4728.5; DB 16; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MQACGSHILCSQQYPAARPAERPGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60
Db 1 MQACGSHILCSQQYPAARPAERPGQVFLKPDPPPPPPQCADSLQDALLSLGSDIV 60

Qy 61 AGLOQAVKEALSAVLPKVTYVTVYLLDGSRLVCEPPHQLPQEGKREAVISRKLCN 120
Db 61 SGLQRAVKEALSAVLPKVTYVTVYLLDGSRLVCEPPHQLPQEGKREAVISRKLCN 120
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Qy 121 GLGPSDLPGKPLARLVAPLAPDTQVLVIFLVDKEAGAAVAVILVHCGQLSDNEENSLQAV 180
Db 121 GLGPSDLPGKPLARLVAPLAPDTQVLVIMPLADKEAGAAVAVILVHCGQLSDNEENSLQAV 180
Qy 181 EXHTTIVALKRVQALQOQRESSVAPETONPPBEAAGDQKGGVAYTDDDKRTILQJCGELYDL 240
Db 181 EXHTTIVALKRVQALQOQRESSVAPETONPPBEAAGDQKGGVAYTDDDKRTILQJCGELYDL 240
Qy 241 DASSLQLKVLQYLOQETOQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPPLTTGRLGQV 300
Db 241 DASSLQLKVLQYLOQETOQASRCCLLLVSEDNLQLSCKVIGDKVLEEEISFPPLTTGRLGQV 299
Qy 301 VEDKKSIOQLKOLITSEDMOQLOSMGLGCEVOAMLCVPIVSRATQOVVALACAFNKLGGDLFT 360
Db 300 VEDKKSIOQLKOLITSEDMOQLOSMGLGCEVOAMLCVPIVSRATQOVVALACAFNKLGGDLFT 359
Qy 361 DODEHVIQHCPTHYTSVLTSTLAFOKEOKLKECCALLOVAKNLFTHLDDVSVLQEIIT 420
Db 360 DODEHVIQHCPTHYTSVLTSTLAFOKEOKLKECCALLOVAKNLFTHLDDVSVLQEIIT 419
Qy 421 EARNLSNAEICSVFLLDQNELVAKVFDGGVGEDESVEIRIPADQGIAGHVATTGQILNIP 480
Db 420 EARNLSNAEICSVFLLDQNELVAKVFDGGVGEDESVEIRIPADQGIAGHVATTGQILNIP 479
Qy 481 DAYAHPLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVVAELVKNKINGPWFSPDEDLATA 540
Db 480 DAYAHPLFYRGVDDSTGFRTRNLCFPIKNEQEVIGVVAELVKNKINGPWFSPDEDLATA 539
Qy 541 PSYICGSIASHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHHDGIQPVAAIDSN 600
Db 540 PSYICGSIASHSLLYKKVNEAQYRSHLANEMMYHMKVSDDEYTKLLHHDGIQPVAAIDSN 599
Qy 601 FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPVHNWM 660
Db 600 FASFTYTPRSIPEDDTSMAILSMLQDMFNINNYKIDCPTLARFCLMVKKGYRDPVHNWM 659
Qy 661 HAFSVSHFCYLLYKNLENTYLEDMEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 720
Db 660 HAFSVSHFCYLLYKNLENTYLEDIEIFALFISCMCHDLDRGTNNSFQVASKSVLAALY 719
Qy 721 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIFKD 780
Db 720 SSEGSMERHFAQAIAIINTHGCNIFDHFSKDYQRMILDMRDIIILATDLAHLRIFKD 779
Qy 781 LQKMAEVGYDRNKKOHSILLCMLTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEVGYDRNKKOHSILLCMLTSCDLSQDTGKWKTRKIAELIYKEFFSQGDLEKA 839
Qy 841 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 900
Db 840 MGNRPMMMDREKAYIPELQISFMEHIAPIYKLLQDLFPKAAELYERVASNRHWTKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYVPLDGDARAPINGCCSLDAE 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVPLDGDTRAPINGCCSLDAE 941

RESULT 6
US-10-686-282-5
; Sequence 5, Application US/10686282
; Publication No. US20050020547A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343D
; CURRENT APPLICATION NUMBER: US/10/686,282
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
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; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-282-5

Query Match 96.3%; Score 4728.5; DB 17; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MGQACGSHILCRSQYPAARPAERGOQVFLKPEPPPPPCADSLQDALLSLGSDIV 60
Db 1 MGQACGSHILCRSQYPAARPAERGOQVFLKPEPPPPPCADSLQDALLSLGSDIV 60

Qy 61 AGLOAVKEALSAPLKPVTYTYLLDGESRLVCEEPHPELPOBQKREAVISRKLGCN 120
Db 61 SGLQAVKEALSAPLPRVETTYTYLLDGESQLVCEDPHPELPOBQKREAVISRKLGCN 120

Qy 121 GLGFSDLPGKPLARLAPLAPDPTQVLVPLVDKAGAAVAVILVHCGQLSNEBWSLQAV 180
Db 121 GLGFSDLPGKPLARLAPLAPDPTQVLVPLVDKAGAAVAVILVHCGQLSNEBWSLQAV 180

Qy 181 EKHTLVALKRVAQLQOERSSVAPENTONPPEEAGDQKGVAYTDORRKLQLCGELYDL 240
Db 181 EKHTLVARRVQVQLQOERAPRAVQNPPEGTAEQKGGAAAYTDRRKLQLCGELYDL 240

Qy 241 DASSLQKVLQYLOQETOASRCCLLLVSEDLNLQLSCKVIGDKVLEEEISPLTTGRGQV 300
Db 241 DASSLQKVLQYLOQETASRCCLLLVSEDLNLQLSCKVIGDKVLEEVSPFL-TGCLGQV 299

Qy 301 VEDKKSILQDLTSEDMOQLSMLGCEVQAMLCVPVISRATDQVVALACAFNKLGGDLFT 360
Db 300 VEDKKSILQDLTSEDVQQLSMLGCELQAMLCVPVISRATDQVVALACAFNKLGGDLFT 359

Qy 361 DQDEHVIQCHFYTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQELIT 420
Db 360 DEDEHVIQCHFYTSVLTSTLAFQEKQKCEQALLQVAKNLFTHLDDVSVLLQELIT 419

Qy 421 EARLNSNAEICSVFLLDQNELVAKVFDGGVVEDESEYRIRPADQGIAGHVATTGQILNIP 480
Db 420 EARLNSNAEICSVFLLDQNELVAKVFDGGVVDDESEYRIRPADQGIAGHVATTGQILNIP 479

Qy 481 DAYAHLFYRGVDDSTGTRTNILCFPIKNENQEVIGVAELVNKINGPWFSPKDEDLATA 540
Db 480 DAYAHLFYRGVDDSTGTRTNILCFPIKNENQEVIGVAELVNKINGPWFSPKDEDLATA 539

Qy 541 FSIYCGISIAHSLLYKKYNEAQYRSHLANEMMYHMKVSDDEYTKLHDGQIPVAADSN 600
Db 540 FSIYCGISIAHSLLYKKYNEAQYRSHLANEMMYHMKVSDDEYTKLHDGQIPVAADSN 599

Qy 601 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKYKGYRDPYHNWM 660
Db 1 MGQACGSHILCRSQYPAARPAERGOQVFLKPEPPPPPCADSLQDALLSLGSDIV 60

Db 600 FASFTYTPRSLPEDDTSMAILSMLQDMNFINNYKIDCPTLARFCLMVKYKGYRDPYHNWM 659
Qy 661 HAFSVSHFCYLLYKNLELTNYLEDEMEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 720
Db 660 HAFSVSHFCYLLYKNLELTNYLEDEIEIFALFISCMCHDLHRGTNNNSFQVASKSVLAALY 719
Qy 721 SSEGSVMERHHAQAIAILNTHGNCIFDHFSRKDYQRMLOIMRDIILATDLAHLRIPKD 780
Db 720 SSEGSVMERHHAQAIAILNTHGNCIFDHFSRKDYQRMLOIMRDIILATDLAHLRIPKD 779
Qy 781 LQKMAEVGYDRNTKQHSHLLCLLMTSCDLSQTKGWTTRKIAELIYKEFFSQGDLEKA 840
Db 780 LQKMAEVGYDRNNKQHSHLLCLLMTSCDLSQTKGWTTRKIAELIYKEFFSQGDLEKA 839
Qy 841 MGNRPMEMDREKAYIPELQISFMEHIAMPTIYKLLQDLFPAKAELYERVASNRHHTWKVS 900
Db 840 MGNRPMEMDREKAYIPELQISFMEHIAMPTIYKLLQDLFPAKAELYERVASNRHHTWKVS 899
Qy 901 HKFTIRGLPSNNSLDFLDEEYVEPDLGAPINGCCSLDAB 942
Db 900 HKFTIRGLPSNNSLDFLDEEYVEPDLGTRAPINGCCSLDAB 941

RESULT 7
US-10-686-349-5
; Sequence 5, Application US/10686349
; Publication No. US20050070499A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Pfizer Limited
; APPLICANT: Maw, Graham Nigel
; APPLICANT: Wayman, Christopher Peter
; TITLE OF INVENTION: Compounds for the Treatment of Female Sexual Dysfunction
; FILE REFERENCE: PC10343C
; CURRENT APPLICATION NUMBER: US/10/686,349
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US 09/708,392
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/175,161
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: GB 9926437.6
; PRIOR FILING DATE: 1999-11-08
; PRIOR APPLICATION NUMBER: GB 0004021.2
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: GB 0013001.3
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0016563.9
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: GB 0017141.3
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/192,962
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/217,479
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/221,014
; PRIOR FILING DATE: 2000-07-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-686-349-5

Query Match 96.3%; Score 4728.5; DB 17; Length 941;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 904; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MGQACGSHILCRSQYPAARPAERGOQVFLKPEPPPPPCADSLQDALLSLGSDIV 60
Db 1 MGQACGSHILCRSQYPAARPAERGOQVFLKPEPPPPPCADSLQDALLSLGSDIV 60


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Db 181 QKGGAAATDRDRKILQLCGELYDLASSLQLKVLQYLQOETRASRCCLLLVSDNLQLSC 240
Qy 277 KVIQDKVLEBISFLTTGRIGQVVEDKKSQQLKDLTSEDNQOQSLMGCCEVQAMLCVPV 336
Db 241 KVIQDKVLEBISFPL-TGCLGQVVEDKKSQQLKDLTSEDNQOQSLMGCCEVQAMLCVPV 299
Qy 337 ISRATDQVVALACAFNKLGGDLFTDQDDEHVHQHCFHYTSTVLTSTLAFQKQKCECOA 396
Db 300 ISRATDQVVALACAFNKLGGDLFTDQDDEHVHQHCFHYTSTVLTSTLAFQKQKCECOA 359
Qy 397 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDDES 456
Db 360 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDDES 419
Qy 457 EIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNIIICFPKKNQBEVI 516
Db 420 EIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNIIICFPKKNQBEVI 479
Qy 517 GVAELVNKINGPWFSPKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 576
Db 480 GVAELVNKINGPWFSPKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 539
Qy 577 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 636
Db 540 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 599
Qy 637 CPTLARFCLMVKKGVRDPPYHNMMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMC 696
Db 600 CPTLARFCLMVKKGVRDPPYHNMMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMC 659
Qy 756 HDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALLNTHGNCIIFDHFSRKDYQ 756
Db 660 HDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALLNTHGNCIIFDHFSRKDYQ 719
Qy 816 RMLDLMRDIILATDLAHLRIIFKDLQKMAEYGVGYDRTNKHSHLLCLLMTSCDLSQTKG 816
Db 720 RMLDLMRDIILATDLAHLRIIFKDLQKMAEYGVGYDRTNKHSHLLCLLMTSCDLSQTKG 779
Qy 876 WKTRKIAELIYKEFPFSGDLEKANGNRPMMMDREKAYIPELQISFMEHIAMPYIKLLQ 876
Db 780 WKTRKIAELIYKEFPFSGDLEKANGNRPMMMDREKAYIPELQISFMEHIAMPYIKLLQ 839
Qy 936 DLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDLDEEYEVPLDQARAPINGC 936
Db 840 DLFPKAAELYERVASNRHWTQVSHKFTIRGLPSNNSLDLDEEYEVPLDQARAPINGC 899
Qy 937 CSLDAB 942
Db 900 CSLDAB 905
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RESULT 12

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US-10-236-417-78
; Sequence 78, Application US/10236417
; Publication No. US20040048256A1
; GENERAL INFORMATION:
; APPLICANT: Agee et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442C
; CURRENT APPLICATION NUMBER: US/10/236,417
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: US60/318,430
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US60/322,781
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/318,184
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/361,663
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US60/396,412
; PRIOR FILING DATE: 2002-07-17
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; PRIOR APPLICATION NUMBER: US60/322,636
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,817
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/322,816
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US60/323,519
; PRIOR FILING DATE: 2001-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: Custom
; SEQ ID NO 78
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-417-78
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Query Match 91.2%; Score 4480.5; DB 15; Length 920;
Best Local Similarity 95.0%; Pred. No. 0;
Matches 861; Conservative 19; Mismatches 25; Indels 1; Gaps 1;

Qy 37 PPPQPCADSLQDALLSLGSDVIDAGLQQAQKESAVLPKVTYTYTYLLDGESERLVCEE 96
Db 16 PGPPGSRDRDLLEDALLSLGSDVIDISGLQRAVKEALSAPVETVYTYTYLLDGESERLVCEE 75
Qy 97 PPHELPOGKGVREAVISRKRLGCGNGLGSPDLPGKPLARLVAPLAPDPTOVVLVPLVDKEAG 156
Db 76 PPHELPOGKGVREAVISRKRLGCGNGLGSPDLPGKPLARLVAPLAPDPTOVVLVPLVDKEAG 135
Qy 157 AVAAVILVHCQSLSDNEEWSLQAVEKHTLVALKRVQALQQRSESVAPETQNPPEEAAGD 216
Db 136 AVAAVILVHCQSLSDNEEWSLQAVEKHTLVALKRVQALQQRSESVAPETQNPPEEAAGD 195
Qy 217 QKGGVATTQDRKILQLCGELYDLASSLQLKVLQYLQOETRASRCCLLLVSDNLQLSC 276
Db 196 QKGGAAATDRDRKILQLCGELYDLASSLQLKVLQYLQOETRASRCCLLLVSDNLQLSC 255
Qy 277 KVIQDKVLEBISFPLTTGRIGQVVEDKKSQQLKDLTSEDNQOQSLMGCCEVQAMLCVPV 336
Db 256 KVIQDKVLEBISFPL-TGCLGQVVEDKKSQQLKDLTSEDNQOQSLMGCCEVQAMLCVPV 314
Qy 337 ISRATDQVVALACAFNKLGGDLFTDQDDEHVHQHCFHYTSTVLTSTLAFQKQKCECOA 396
Db 315 ISRATDQVVALACAFNKLGGDLFTDQDDEHVHQHCFHYTSTVLTSTLAFQKQKCECOA 374
Qy 397 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDDES 456
Db 375 LLQVAKNLFTHLDDVSVLLQBIITEARNLSNAEICSVFLLDQNELVAKVFDGQVVDDES 434
Qy 457 EIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNIIICFPKKNQBEVI 516
Db 435 EIRIPADQGIAGHVATTGQILNIPDAYAHPFLFYRGVDDSTGFRTRNIIICFPKKNQBEVI 494
Qy 517 GVAELVNKINGPWFSPKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 576
Db 495 GVAELVNKINGPWFSPKPEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYHM 554
Qy 577 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 636
Db 555 KVSDEYTKLLHDGQIPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFNNYKID 614
Qy 637 CPTLARFCLMVKKGVRDPPYHNMMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMC 696
Db 615 CPTLARFCLMVKKGVRDPPYHNMMHAFSVSHFCVLLYKNLELTNYLEDMEIFALFISCMC 674
Qy 697 HDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALLNTHGNCIIFDHFSRKDYQ 756
Db 675 HDLDRGTNNNSFQVASKSVLAALYSSEGSVMERHHFAQAIALLNTHGNCIIFDHFSRKDYQ 734
Qy 757 RMLDLMRDIILATDLAHLRIIFKDLQKMAEYGVGYDRTNKHSHLLCLLMTSCDLSQTKG 816
Db 735 RMLDLMRDIILATDLAHLRIIFKDLQKMAEYGVGYDRTNKHSHLLCLLMTSCDLSQTKG 794
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QY 817 WKTTRKIAELIYKEPFSQDLEKAMGNRPMMMDREKAYIPPELOISFMEHIAMPIYKLIQ 876
DB 795 WKTTRKIAELIYKEPFSQDLEKAMGNRPMMMDREKAYIPPELOISFMEHIAMPIYKLIQ 854
QY 877 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDLDEEVEVPDLDCGARAPINGC 936
DB 855 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDLDEEVEVPDLDCGARAPINGC 914
QY 937 CSLDAE 942
DB 915 CSLDAE 920

RESULT 13
US-10-094-989-2
; Sequence 2, Application US/10094989
; Publication No. US20020115179A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063DIV
; CURRENT APPLICATION NUMBER: US/10/094,989
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/754,250
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 920
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-989-2

Query Match 91.1%; Score 4474.5; DB 13; Length 920;
Best Local Similarity 94.9%; Pred. No. 0;
Matches 860; Conservative 19; Mismatches 26; Indels 1; Gaps 1;

QY 37 PPPQPCADSLQDALLSLGSLVDVAGLQAAVKEALSAVLPKVETVYTYLLDGESRLVCEE 96
DB 16 PGPQSGRRDLLEALLSLGSLVDISGLQAAVKEALSAVLPKVETVYTYLLDGESRLVCEE 75
QY 97 PPHELPOBQKVREAVISRRKLCNGLGSLDLPKGLARLAPLAPDTQVLVPLVDEKAG 156
DB 76 PPHELPOBQKVREAVISRRKLCNGLGSLDLPKGLARLAPLAPDTQVLVPLVDEKAG 135
QY 157 AVAAVILVHCGQLSDNEBSLQAAVKEHTLVALKRVQALQOQRESSVAPRATQNPPEAAGD 216
DB 136 AVAAVILVHCGQLSDNEBSLQAAVKEHTLVALKRVQALQOQRESSVAPRATQNPPEAAGD 195
QY 217 OKGGVAYTDDRKILQCGELYDLDASSLQKLVQLOQETOASRCCLLLVSEDLNLQSC 276
DB 196 OKGGAAVYDTRDKILQCGELYDLDASSLQKLVQLOQETRASRCCLLLVSEDLNLQSC 255
QY 277 KVIGKVLBEERTSFPLTTRGLQGVVEDKKSIOQLDTSDEMQLQSLGCEVQAMLCVPV 336
DB 256 KVIGKVLBEERTSFPLTTRGLQGVVEDKKSIOQLDTSDEMQLQSLGCEVQAMLCVPV 314
QY 337 ISRATDQVVALACAFNKLGGDLFTDDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 396
DB 315 ISRATDQVVALACAFNKLGGDLFTDDEHVIQHCFTYTSVLTSTLAFQKQKLCCEQA 374
QY 397 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFLLDQNELVAKVFDGGVDESEY 456
DB 375 LLOVAKNLFTHLDDVSVLLQEIITEARNLSNAEICSFLLDQNELVAKVFDGGVDESEY 434
QY 457 EIRIPADQGIAGHVAATTGQILNIPDAYAHLPIYRGVDDSTGPRTRNIIICFPKIKNEQVI 516
DB 435 EIRIPADQGIAGHVAATTGQILNIPDAYAHLPIYRGVDDSTGPRTRNIIICFPKIKNEQVI 494
QY 517 GVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYTHM 576
DB 517 GVAELVNKINGPWFSKFDEDLATAFSIYCGISIAHSLLYKKVNEAQYRSHLANEMMYTHM 554
QY 577 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKID 636
DB 555 KVSDEYTKLLHDGIQPVAAIDSNFASFTYTPRSLPEDDTSMALLSMLQDMNFINNYKID 614
QY 637 CPTLARFCLMWKKGVRDPPYHNMHAFSVSHFCYLLYKULELTNYLEDMEIEIHALFISCMC 696
DB 615 CPTLARFCLMWKKGVRDPPYHNMHAFSVSHFCYLLYKULELTNYLEDMEIEIHALFISCMC 674
QY 697 HDLDRGTNNNSFOVASKSVLAALYSSEGVSMRHHFAQAIAIINTHGCNIPOHPSRDKYQ 756
DB 675 HDLDRGTNNNSFOVASKSVLAALYSSEGVSMRHHFAQAIAIINTHGCNIPOHPSRDKYQ 734
QY 757 RMLDLMRDIIILATDLAHLRIKQIAEVEGYDRTNKHSHLSLLCLLMTSCDLSQTKG 816
DB 735 RMLDLMRDIIILATDLAHLRIKQIAEVEGYDRTNKHSHLSLLCLLMTSCDLSQTKG 794
QY 817 WKTTRKIAELIYKEPFSQDLEKAMGNRPMMMDREKAYIPPELOISFMEHIAMPIYKLIQ 876
DB 795 WKTTRKIAELIYKEPFSQDLEKAMGNRPMMMDREKAYIPPELOISFMEHIAMPIYKLIQ 854
QY 877 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDLDEEVEVPDLDCGARAPINGC 936
DB 855 DLFPKAAELYERVASNRHWTKVSHKFTIRGLPSNNSLDLDEEVEVPDLDCGARAPINGC 914
QY 937 CSLDAE 942
DB 915 CSLDAE 920
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RESULT 14

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US-10-108-260A-2928
; Sequence 2928, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2928
; LENGTH: 950
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-2928

Query Match 87.0%; Score 4272.5; DB 15; Length 950;
Best Local Similarity 92.9%; Pred. No. 0;
Matches 827; Conservative 21; Mismatches 33; Indels 9; Gaps 2;

QY 1 MGQACGHILCRSQOYPAAR-----PABPRGQOVFLKPDPEPPPPQPCADSLQDALL 52
DB 62 VGPSTWTHSGASRSSRSTRRRRRSHAPTACRRGQOVFLKPDPEPPPPQPCADSLQDALL 121
QY 53 SLGSLVIDVAGLQAAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPOBQKVREAVI 112
DB 122 SLGSLVIDISGGLQAAVKEALSAVLPKVETVYTYLLDGESRLVCEEPPHELPOBQKVREAVI 181
QY 113 SRKRLGNCGLGPSDLPGKPLARLAPLAPDTQVLVPLVDEKAGAAVAVILVHCGQLSDN 172
DB 182 SQKRLGNCGLGFSDDLPGKPLARLAPLAPDTQVLVPLVDEKAGAAVAVILVHCGQLSDN 241
QY 173 EWSLQAVKEHTLVALKRVQALQOQRESSVAPRATQNPPEAAGDQKGVAYTDDRKILQ 232
DB 242 EWSLQAVKEHTLVALKRVQALQOQRESSVAPRATQNPPEAAGDQKGVAYTDDRKILQ 301
QY 233 LCGELYDLDASSLQKLVQLOQETOASRCCLLLVSEDLNLQSCVKVIGDVLBEERTSFPL 292
DB 302 LCGELYDLDASSLQKLVQLOQETRASRCCLLLVSEDLNLQSCVKVIGDVLBEERTSFPL 361
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Qy	293	TTGRLGQVVEDKKS	IQLKDLTSDMDQOQSMGLGCEVOAMLCVPVTSRATDQVVALACAFN	352	
Db	362	-TGC	LGQVVEBKKS	IQLKDLTSDMDQOQSMGLGCEVOAMLCVPVTSRATDQVVALACAFN	420
Qy	353	KGGDLFTDQDEHVI	QHCFTYSTVLTSTLAFQKEQKLKCECOALLOQVAKNLFTHLDDVS	412	
Db	421	KLEGDLFTDEHVI	QHCFTYSTVLTSTLAFQKEQKLKCECOALLOQVAKNLFTHLDDVS	480	
Qy	413	VLLQEIITEARNLSNAE	ICSVFLLDQNELVAKVFDGGVVEDESVEIRIPADQGIAGHVAT	472	
Db	481	VLLQEIITEARNLSNAE	ICSVFLLDQNELVAKVFDGGVVEDESVEIRIPADQGIAGHVAT	540	
Qy	473	TGQILNI	PDAYAHPLFYRGVDDSTGFRTRNLCPPIKNENQEVIGVABLNVKINGPWFSK	532	
Db	541	TGQILNI	PDAYAHPLFYRGVDDSTGFRTRNLCPPIKNENQEVIGVABLNVKINGPWFSK	600	
Qy	533	FDEDLATAFSYCGISIAH	SLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQ	592	
Db	601	FDEDLATAFSYCGISIAH	SLLYKKNVNAQYRSHLANEMMYHMKVSDDEYTKLLHDGIQ	660	
Qy	593	PVAIDSNFASFTYTPRSL	PEDDTSMAILSMQDMNFNNKYKIDCPTLARCLMVKKGYR	652	
Db	661	PVAIDSNFASFTYTPRSL	PEDDTSMAILSMQDMNFNNKYKIDCPTLARCLMVKKGYR	720	
Qy	653	DPYHNMWHA	FSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSFQVAS	712	
Db	721	DPYHNMWHA	FSVSHFCYLLYKNLELTNYLEDMEIFALFISCMCHDLDRGTNNSFQVAS	780	
Qy	713	KSVLAALYSSEGS	VMERHHFAQAIATLNTGNCNIPDFHSRKYQRMULDMDRIILATDLA	772	
Db	781	KSVLAALYSSEGS	VMERHHFAQAIATLNTGNCNIPDFHSRKYQRMULDMDRIILATDLA	840	
Qy	773	HLHRIFKDLQMAE	VGYDRTKQKHSLLLCLLMTSCDLSQDKGKWKTRKIAELIYKEFF	832	
Db	841	HLHRIFKDLQMAE	VGYDRTKQKHSLLLCLLMTSCDLSQDKGKWKTRKIAELIYKEFF	900	
Qy	833	SGQDLEKANGNRP	MEMDMREKAYIPELOISMEHIAMPIYKLLQDLRPPKA	882	
Db	901	SGQDLEKANGNRP	MEMDMREKAYIPELOISMEHIAMPIYKLLQDLRPPKA	950	

RESULT 15

US-10-104-047-2944
; Sequence 2944, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2944
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2944

Query Match	71.0%	Score	3484.5;	DB	15;	Length	786;		
Best Local Similarity	94.1%	Fred.	No. 7e-274;						
Matches	672;	Conservative	19;	Mismatches	22;	Indels	1;	Gaps	1;
Qy	37	PPPPQPCADSLQDALL	SLGVSVIDVAGLQQAQVKEALSAVLPKVETVYTYLLDGSRLVCEE	96					
Db	16	PGPGSRDRDL	EALLSLGVSVIDISGLQRAVKEALSAVLPRVETVYTYLLDGSRLVCEE	75					
Qy	97	PPHELPOGKGVREAVIS	KRLGCGNLGSPDLPGKPLARLVAPLAPDQVVLVPLVDEKAG	156					
Db	76	PPHELPOGKGVREAVIS	KRLGCGNLGSPDLPGKPLARLVAPLAPDQVVLVPLVDEKAG	135					

Qy	157	AVAAVILVHCQLSDNE	WSLQAVEKHTLVALKRVOALQOQRESSVAPATQNPPEAAAGD	216	
Db	136	AVAAVILVHCQLSDNE	WSLQAVEKHTLVALKRVOALQOQRESSVAPATQNPPEAAAGD	195	
Qy	217	QKGGVAYTDQDRKIL	QCGELYDLDASSLQKLVLOYLQOETOASRCCLLLVSDNQLQSC	276	
Db	196	QKGGAAVTDQDRKIL	QCGELYDLDASSLQKLVLOYLQOETOASRCCLLLVSDNQLQSC	255	
Qy	277	KVIGDKVLEBEIS	PLTGRLGQVVEDKKS	IQLKDLTSDMDQOQSMGLGCEVOAMLCVPV	336
Db	256	KVIGDKVLEBEIS	PLTGRLGQVVEDKKS	IQLKDLTSDMDQOQSMGLGCEVOAMLCVPV	314
Qy	337	ISRATDQVVALACAFN	KLGDLFTDQDEHVIQHCFTYSTVLTSTLAFQKEQKLKCECOA	396	
Db	315	ISRATDQVVALACAFN	KLGDLFTDQDEHVIQHCFTYSTVLTSTLAFQKEQKLKCECOA	374	
Qy	397	LLQVAKNLFTHLDD	VSVLLQBEIITEARNLSNAE	ICSVFLLDQNELVAKVFDGGVVEDES	456
Db	375	LLQVAKNLFTHLDD	VSVLLQBEIITEARNLSNAE	ICSVFLLDQNELVAKVFDGGVVEDES	434
Qy	457	EIRIPADQGIAGHVAT	TGQILNI	PDAYAHPLFYRGVDDSTGFRTRNLCPPIKNENQEV	516
Db	435	EIRIPADQGIAGHVAT	TGQILNI	PDAYAHPLFYRGVDDSTGFRTRNLCPPIKNENQEV	494
Qy	517	GVAELVNKINGPWFS	KFDEDLATAFSYCGISIAH	SLLYKKNVNAQYRSHLANEMMYHMH	576
Db	495	GVAELVNKINGPWFS	KFDEDLATAFSYCGISIAH	SLLYKKNVNAQYRSHLANEMMYHMH	554
Qy	577	KVSDDEYTKLLHDGI	QPVAAIDSNFASFTYTPRSL	PEDDTSMAILSMQDMNFNNKYKID	636
Db	555	KVSDDEYTKLLHDGI	QPVAAIDSNFASFTYTPRSL	PEDDTSMAILSMQDMNFNNKYKID	614
Qy	637	CPTLARCLMVKKGYR	PPYHNMWHA	FSVSHFCYLLYKNLELTNYLEDMEIFALFISCMC	696
Db	615	CPTLARCLMVKKGYR	PPYHNMWHA	FSVSHFCYLLYKNLELTNYLEDMEIFALFISCMC	674
Qy	697	HDLDRGTNNS	FOVASKSVLAALYSSEGS	VMERHHFAQAIATLNTGNCNIPDFH	750
Db	675	HDLDRGTNNS	FOVASKSVLAALYSSEGS	VMERHHFAQAIATLNTGNCNIPDFH	728

Search completed: June 26, 2005, 12:41:01
Job time : 120.308 secs